

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 21:08:15 ; Search time 6122.4 Seconds  
(without alignments)  
10898.153 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pt.\*
- 10: gb\_ro.\*
- 11: gb\_scs.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1328.4	96.5	1453	6	AX056745 Sequence
3	1049.2	76.2	1444	6	AX056747 Sequence
4	1039	75.5	1359	6	AX056739 Sequence
5	1032.4	75.0	1389	6	AX056741 Sequence
6	987.4	71.7	1674	6	AX056737 Sequence
7	982.4	71.3	1704	6	AX056743 Sequence
8	980.8	71.2	1704	6	AX056735 Sequence
9	687.2	49.9	1383	6	AX138526 Sequence
10	686	49.8	2043	6	AR112718 Sequence
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ALIGNMENTS

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DEFINITION	AX056749				
ACCESSION	AX056749.1				
VERSION	GI:12309728				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE 1  
Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D.  
Modified chimeric polypeptides with improved pharmacokinetic properties  
Patent: WO 0075319-A 15 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
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ORIGIN

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Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 11 from Patent WO0075319.
ACCESSION AX056745
VERSION AX056745.1 GI:12309724
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic
properties
JOURNAL Patent: WO 0075319-A 11 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES
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RESULT 3
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LOCUS AX056747 1444 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 13 from Patent WO0075319.
ACCESSION AX056747
VERSION AX056747.1 GI:12309726
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic
properties
JOURNAL Patent: WO 0075319-A 13 14-DEC-2000;
REGENBRON PHARMACEUTICALS, INC. (US)
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Qy	661	AAGAACAGCACATTTGTTCAGGGTCCATGAAAGAGCAAACTCAACATGCCACCGTGC	720
Db	643	GATAAGCAGGCCGCGGAGCCCAAACTCTGTGACAAACTCAACATGCCACCGTGC	702
Qy	721	CAGCACCTGAATCTCTGGGGGAGCGTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGAC	780
Db	703	CCAGCACCTGAATCTCTGGGGGAGCGTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGAC	762
Qy	781	ACCTCATGATCTCCCGGACCCCTCAGGTCACATGCTGGTGGTGGAGCTGAGCCACGAA	840
Db	763	ACCTCATGATCTCCCGGACCCCTCAGGTCACATGCTGGTGGTGGAGCTGAGCCACGAA	822
Qy	841	GACCTCAGGTCAGTTCAACTGGTACCTGAGCGCGCTGGAGGTGCATAATGCCAAGACA	900
Db	823	GACCTCAGGTCAGTTCAACTGGTACCTGAGCGCGCTGGAGGTGCATAATGCCAAGACA	882
Qy	901	AAGCCGCGGAGGAGCAGTACAAAGCAGCTACCTGTGGTCAGCGTCTCACCCTGCTG	960
Db	883	AAGCCGCGGAGGAGCAGTACAAAGCAGCTACCTGTGGTCAGCGTCTCACCCTGCTG	942
Qy	961	CACCAAGGACTGCTGAATGGCAAGGATACAGTGCAGAGTCTCCAAACAAAGCCCTCCCA	1020
Db	943	CACCAAGGACTGCTGAATGGCAAGGATACAGTGCAGAGTCTCCAAACAAAGCCCTCCCA	1002
Qy	1021	GCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGAGAACCCACAGGTGTAC	1080
Db	1003	GCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGAGAACCCACAGGTGTAC	1062
Qy	1081	ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCTGCTGTC	1140
Db	1063	ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCTGCTGTC	1122
Qy	1141	AAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGCGGAGAAC	1200
Db	1123	AAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGCGGAGAAC	1182
Qy	1201	AACTACAAGACCAACCCCTGCTGCTGAGTCCGACCGCTCTCTCTCTACAGCAAG	1260
Db	1183	AACTACAAGACCAACCCCTGCTGCTGAGTCCGACCGCTCTCTCTCTACAGCAAG	1242
Qy	1261	CTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGATGAT	1320
Db	1243	CTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGATGAT	1302
Qy	1321	GAGGCTCTGCACAAACCATCTACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1377
Db	1303	GAGGCTCTGCACAAACCATCTACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1359

RESULT 5  
AX056741  
LOCUS AX056741 1389 bp DNA linear PAT 17-JAN-2001  
DEFINITION Sequence 7 from Patent WO0075319.  
ACCESSION AX056741

VERSION	AX056741.1	GI:12309720
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D. Modified chimeric polypeptides with improved pharmacokinetic properties Patent: WO 0075319-A 7 14-DEC-2000; REGENERON PHARMACEUTICALS, INC. (US) Location/Qualifiers 1. .1389 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 1. .1389 /note="unnamed protein product"	
AUTHORS	Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.	
TITLE	Modified chimeric polypeptides with improved pharmacokinetic properties	
JOURNAL	REGENERON PHARMACEUTICALS, INC. (US)	
FEATURES	source	
CDS	EGRELVPICRVTSNITVTKKFDLIPDGKRIIWDNRKGFIIISNATYKBIIGLLTC EATVNGHLYKTNLYTHRTQITIIIDQISTPRPVKLLRGLTATPLNTRVQMT WSYDEKKNKASVRRRIDQNSHANI FVSVLTIDKQNKDKGLVTCRVRSPSPKSVN TSVHIYDKPGEPKSCDKTHCPCPAPBLGGSPVFLPPKDKDLMISRTPEVTC VVDVSHEDBEVKENWYDGVENHNAKTKRBEQYNSYRVRVSVLTVLHQDLNGKEY KCRVSKALPAPIEKTISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVGFYPSDI AVVESNGKPPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFCVSMHEALHNI YTQKSLSLSPGK"	
ORIGIN	Query Match 75.0%; Score 1032.4; DB 6; Length 1389; Best Local Similarity 85.5%; Pred. No. 1.2e+29; Matches 1201; Conservative 0; Mismatches 161; Indels 42; Gaps 3;	
Qy	1	ATGTCAGTACTGCGGACACCGGGTCTGCTGTGCGCGCTGCTCAGCTGCTGCTCTCTC 60
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Qy	61	ACAGATCTAGTTCGGAGGTGATACCGGTAGACCTTTCTGTAGAGATGACAGTGAATC 120
Db	61	ACAGATCTAGTTCGGAGGTGATACCGGTAGACCTTTCTGTAGAGATGACAGTGAATC 111
Qy	121	CCCCAAATTATACATGACTGAAGGAGGAGTCTGTCATTCCTCCGCGGTACGTCA 180
Db	112	CCCCAAATTATACATGACTGAAGGAGGAGTCTGTCATTCCTCCGCGGTACGTCA 171
Qy	181	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGTAGGAAAA 240
Db	172	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGTAGGAAAA 231
Qy	241	CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAATCAACAGTCAAAAGAAATA 300
Db	232	CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAATCAACAGTCAAAAGAAATA 291
Qy	301	GGGCTTCGACCTGTGAAGCAGAGTCAATGGGCATTTGTATATAGACAACTATCTACA 360
Db	292	GGGCTTCGACCTGTGAAGCAGAGTCAATGGGCATTTGTATATAGACAACTATCTACA 351
Qy	361	CATCGACAAACCAATCAATCATAGATGTGGTCTGTAGTCCGTCTCATGGAAATTGAACCTA 420
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Qy	421	TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480
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Qy	481	GACTTCAACTGGGAATACCTTCTTCGAGCATCAGCATATAGAAACTTGTAAACCGAGAC 540
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QY 1072 CAGGTGTACACCTGCCCCATCCCGGGATGAGTGAACAAGAACAGAGTCAAGCTGACC 1131
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DB 1579 TACAGCAAGCTCAGCGTGAACAAGAGCAGGTGGCAGAGGGAACGTCTTCTCATGCTCC 1638
QY 1312 GTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGT 1371
DB 1639 GTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGT 1698
QY 1372 AAATGA 1377
DB 1699 AAATGA 1704

RESULT 9
AX338526 LOCUS AX338526 1383 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 17 from Patent WO0185789.
ACCESSION AX338526
VERSION AX338526.1 GI:18128935
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Roczniak,S., Dubois-Stringfellow,N.A. and Zolotorov,A.
TITLE Method of regulating angiogenesis using ryk protein
JOURNAL Patent: WO 0185789-A 17 15-NOV-2001;
Bayer Corporation (US)
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/db_xref="taxon:32630"
/note="fusion of human cDNA and Fc tag coding sequence"

ORIGIN
Query Match 49.9%; Score 687.2; DB 6; Length 1383;
Best Local Similarity 99.6%; Pred. No. 3.1e-149;
Matches 689; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 686 ATGAAAGGACAAACTCACATGCCACCGTGGCCAGCAGCCTGAATCTCTGGGGGAC 745
DB 692 ATGATGATGACAAAACTCACATGCCACCGTGGCCAGCAGCCTGAATCTCTGGGGGAC 751
QY 746 CGTCACTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTG 805
DB 752 CGTCACTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTG 811
QY 806 AGTTCACATGCTGTGTGAGCGTGAAGCAGCAAGACCCCTGAGGTCAAGTTCAACTGGT 865
DB 812 AGTTCACATGCTGTGTGAGCGTGAAGCAGCAAGACCCCTGAGGTCAAGTTCAACTGGT 871
QY 866 ACCTGGAGCGGTGGAGGTGCATATGCCAGACAAAGCCCGGGAGGAGCAGTACACA 925
DB 872 ACCTGGAGCGGTGGAGGTGCATATGCCAGACAAAGCCCGGGAGGAGCAGTACACA 931
QY 926 GCACGTACCGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACCAAGAGCTGGGTGAATGSCAAG 985
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DB 932 GCACGTACCGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACCAAGAGCTGGGTGAATGSCAAG 991
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DB 992 AGTACAAGTGAAGGTCTTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCA 1051
QY 1046 AAGCCAAAGGCGCAGCCCGAGAACACACAGGTGTACACCTGCCCTCCCATCCCGGGATGAGC 1105
DB 1052 AAGCCAAAGGCGCAGCCCGAGAACACACAGGTGTACACCTGCCCTCCCATCCCGGGATGAGC 1111
QY 1106 TGACCAAGAACCAAGGTCAAGCTGACCTGCTTGGTCAAAAGGCTTCTATCCAGCGACATCG 1165
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QY 1166 CCGTGGAGTGGGAGAGCAATGGGAGCCGAGAGAACATAAGACACGCTTCCCGTGC 1225
DB 1172 CCGTGGAGTGGGAGAGCAATGGGAGCCGAGAGAACATAAGACACGCTTCCCGTGC 1231
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DB 1352 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1383

RESULT 10
AR112718 LOCUS AR112718 2043 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 14 from patent US 6130202.
ACCESSION AR112718
VERSION AR112718.1 GI:14092618
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2043)
AUTHORS Greve,J.M. and McClelland,A.
TITLE Antiviral methods
JOURNAL Patent: US 6130202-A 14 10-OCT-2000;
FEATURES Location/Qualifiers
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Best Local Similarity 95.9%; Pred. No. 6e-149;
Matches 704; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 644 GTGGGCTGTATGACCAAGAGAACAGCACATTTGTAGGGTCCATGAAAGAGCAAAACTC 703
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QY 704 ACACATGCCACCGTGGCCAGCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCC 763
DB 1370 ACATATGCCACCGTGGCCAGCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCC 1429
QY 764 CCCCAGAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGG 823
DB 1430 CCCCAGAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGG 1489
QY 824 TGGAGCTGAGGACCAAGACCCCTGAGGTCAAGTTCAATGCTAGCTGAGCGCGGTGAGG 883
DB 1490 TGGAGCTGAGGACCAAGACCCCTGAGGTCAAGTTCAATGCTAGCTGAGCGCGGTGAGG 1549
QY 884 TGCAATATGCCAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTACCGTGTGGTCA 943
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PC C12N15/09, A61K38/48, A61K39/00, A61K39/395, A61K48/00, A61P1/04, PC  
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PC A61P3/10, A61P7/06, A61P9/02, A61P11/02, A61P11/06, A61P17/00, PC  
A61P17/06,  
PC A61P19/02, A61P21/02, A61P21/04, A61P25/00, A61P35/00, A61P37/02,  
PC A61P37/06,  
PC C07K14/705, C07K16/46, C07K19/00, C12N5/10, C12N15/00, C12N5/00, PC  
A61K37/02  
CC Description of Sequence: Recombinant Polynucleotide FH Key  
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Query Match 49.7%; Score 684; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 1.7e-148; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0;

Qy 694 GACAAAACCTCACATGCCCGTGGCCAGCACCTGAACTCTCTGGGGGAGCCGTCAGTC 753  
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Qy 754 TTCCTCTTCCCTCCCAAAACCCAGAGACACCTCTATGATCTCCCGGACCCCTGAGGTACA 813  
Db 388 TTCCTCTTCCCTCCCAAAACCCAGAGACACCTCTATGATCTCCCGGACCCCTGAGGTACA 447  
Qy 814 TGCCTGTGTGGAGCTGAGCAGCAGACACCTCTGAGGTCAAGTTCAACTGCTGAGTGGAC 873  
Db 448 TGCCTGTGTGGAGCTGAGCAGCAGACACCTCTGAGGTCAAGTTCAACTGCTGAGTGGAC 507  
Qy 874 GGCCTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTCAC 933  
Db 508 GGCCTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTCAC 567  
Qy 934 CGTGTGTGAGGTCTCAGCGTCTGCAACAGACCTGGCTGATGGCAAGGATACAG 993  
Db 568 CGTGTGTGAGGTCTCAGCGTCTGCAACAGACCTGGCTGATGGCAAGGATACAG 627  
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Qy 1114 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 1173  
Db 748 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 807  
Qy 1174 TGGGAGAGCAATGGCAGCCGAGAACCAACTACAGACACGCTCCCGTCTGACTCC 1233  
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LOCUS AR275187 1019 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6506891.  
ACCESSION AR275187  
VERSION AR275187.1 GI:29708174  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1019)  
AUTHORS Tao, W., Wong, S., Hickey, W.F., Hamman, J.P. and Baetge, E.E.  
TITLE Cell surface molecule-induced macrophage activation  
JOURNAL Patent: US 6506891-A 1 14-JAN-2003;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 49.7%; Score 684; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 1.7e-148; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0;

Qy 694 GACAAAACCTCACATGCCCGTGGCCAGCACCTGAACTCTCTGGGGGAGCCGTCAGTC 753  
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Qy 754 TTCCTCTTCCCTCCCAAAACCCAGAGACACCTCTATGATCTCCCGGACCCCTGAGGTACA 813  
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Qy 814 TGCCTGTGTGGAGCTGAGCAGCAGACACCTCTGAGGTCAAGTTCAACTGCTGAGTGGAC 873  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-009-852-15

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	1049.2	76.2	1444	5	AAA91075
6	1049.2	76.2	1444	6	ABQ74609
7	1039	75.5	1359	5	AAA91071
8	1039	75.5	1359	6	ABQ74605
9	1032.4	75.0	1389	5	AAA91072
10	1032.4	75.0	1389	6	ABQ74606
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35	684	49.7	705	11	AD131897	AD131897 Human CDN
36	684	49.7	705	12	ADL46173	ADL46173 Human imm
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38	684	49.7	762	10	AA53735	AA53735 Human wil
39	684	49.7	762	10	AA53755	AA53755 Human mod
40	684	49.7	762	10	AA53760	AA53760 Human mod
41	684	49.7	993	12	ADM68909	ADM68909 Human Igg
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43	684	49.7	1002	12	ADN97484	ADN97484 Artificial
44	684	49.7	1019	3	AAA53126	AAA53126 Human TR-
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#### ALIGNMENTS

RESULT 1

AAA91076

ID AAA91076 standard; DNA; 1377 BP.

AC AAA91076;

DT 05-APR-2001 (first entry)

DE Flt1 receptor fusion protein VEGFR1R2-FcDeltaC2 (a) coding sequence.

XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

KW plasma leakage; vascular permeability; Igg Fc region; ss.

KW plasma leakage; vascular permeability; Igg Fc region; ss.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

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XX Unidentified.

XX Unidentified.

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XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.

XX Unidentified.



CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
XX permeability in a mammal

SQ Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1377; DB 5; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGTCACGCTACTGGGACACCGGGCTCTGCTGTGGCGCTGCTCAGCTGTCTCTTC 60
DB 1 ATGGTCACGCTACTGGGACACCGGGCTCTGCTGTGGCGCTGCTCAGCTGTCTCTTC 60

QY 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120
DB 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120

QY 121 CCCGAAATATACATGACTGATGAAGGAAGGAGCTCGTCATTCCTGCGGGTTACGTCA 180
DB 121 CCCGAAATATACATGACTGATGAAGGAAGGAGCTCGTCATTCCTGCGGGTTACGTCA 180

QY 181 CCTAACATCACTGTTACTTTTAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAA 240
DB 181 CCTAACATCACTGTTACTTTTAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAA 240

QY 241 CGCATAAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300
DB 241 CGCATAAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300

QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 360
DB 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 360

QY 361 CATGCACAAACCAATACATCATAGATGCTGTTCTGAGTCGCTCTCATGGNAATGAACTA 420
DB 361 CATGCACAAACCAATACATCATAGATGCTGTTCTGAGTCGCTCTCATGGNAATGAACTA 420

QY 421 TCTGTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATAATGTGGGATT 480
DB 421 TCTGTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATAATGTGGGATT 480

QY 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTGTAAACCCGAGAC 540
DB 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTGTAAACCCGAGAC 540

QY 541 CTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTGACACCTTAACTATAGATGGT 600
DB 541 CTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTGACACCTTAACTATAGATGGT 600

QY 601 GTAAACCCGAGTACCAAGAGTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660
DB 601 GTAAACCCGAGTACCAAGAGTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660

QY 661 AAGAACAGCAATTTGTGAGGGTCCATGAAAGGACAAACTCACAATGCCACCCGTCG 720
DB 661 AAGAACAGCAATTTGTGAGGGTCCATGAAAGGACAAACTCACAATGCCACCCGTCG 720

QY 721 CCAGACCTGAATCTCCGGGAGCCGTCAGTCTCATATGCTGTGGTGGAGCTGAGCCAGAA 840
DB 721 CCAGACCTGAATCTCCGGGAGCCGTCAGTCTCATATGCTGTGGTGGAGCTGAGCCAGAA 840

QY 841 GACCTGAGGTCAAGTTCAACTGGTACGTGGAACGGGCTGGAGGTGCATATGCAAGACA 900
DB 841 GACCTGAGGTCAAGTTCAACTGGTACGTGGAACGGGCTGGAGGTGCATATGCAAGACA 900
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QY 901 AAGCCGCGGAGGAGCAGTACAAACAGCACGTACCGTGTGGTCTCAGCGTCTCACCGTCTG 960
DB 901 AAGCCGCGGAGGAGCAGTACAAACAGCACGTACCGTGTGGTCTCAGCGTCTCACCGTCTG 960

QY 961 CACCAGACTCGGTGTAATGGCAAGGAGTACAAGGTGCAAGGTCTTCCAAACAAAGCCCTCCA 1020
DB 961 CACCAGACTCGGTGTAATGGCAAGGAGTACAAGGTGCAAGGTCTTCCAAACAAAGCCCTCCA 1020

QY 1021 GCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAAACCAACAGGTGTAC 1080
DB 1021 GCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAAACCAACAGGTGTAC 1080

QY 1081 ACCCTGCCCCCATCCCGGGATGAGCTACCAAGAACCAAGGTGAGCTGCTGCTCGTGC 1140
DB 1081 ACCCTGCCCCCATCCCGGGATGAGCTACCAAGAACCAAGGTGAGCTGCTGCTCGTGC 1140

QY 1141 AAAGGCTTCTATCCACGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAAC 1200
DB 1141 AAAGGCTTCTATCCACGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAAC 1200

QY 1201 AACTAAGAACACCGCTCCCGTGTGGAATCCGACGGCTCTTCTTCTCTACAGCAAG 1260
DB 1201 AACTAAGAACACCGCTCCCGTGTGGAATCCGACGGCTCTTCTTCTCTACAGCAAG 1260

QY 1261 CTCACCGTGACAAAGAGCAGGTGGCAGAGGGGAACTCTTCTCATGCTCCGCTGATGCAT 1320
DB 1261 CTCACCGTGACAAAGAGCAGGTGGCAGAGGGGAACTCTTCTCATGCTCCGCTGATGCAT 1320

QY 1321 GAGGCTCTGCACAAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377
DB 1321 GAGGCTCTGCACAAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377
```

RESULT 2  
ABQ74610

ID ABQ74610 standard; cdna; 1377 BP.

XX AC ABQ74610;

XX DT 23-OCT-2002 (first entry)

XX DE Modified Flt1 receptor VEGFR1R2-FcDELTA1(a) nucleotide sequence.

XX KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
XX KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
XX KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
XX KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
XX KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
XX KW kidney disease; eye disorder; age-related macular degeneration;  
XX KW diabetic retinopathy; gene; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT CDS 1..1377

XX FT /\*tag= a

XX FT /product= "VEGFR1R2-FcDELTA1(a)"

XX PN WO200260489-A1.

XX PD 08-AUG-2002.

XX PF 28-JAN-2002; 2002WO-US002466.

XX PR 31-JAN-2001; 2001US-00773877.

XX PA (REG-) REGENERON PHARM INC.

XX PI Xia Y, Rudge JS, Yancopoulos GD;

XX XX WPI; 2002-608488/65.

XX DR P-PSDB; ABP52449.

XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.

XX Example 20; Fig 24A-C; 179pp; English.

XX The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes VEGFR1R2-  
CC FCDELTA1(a) which is used in an example from the present invention

XX Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1377; DB 6; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGCTGCTCAGCTGCTGCTTC 60  
DB 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGCTGCTCAGCTGCTGCTTC 60  
QY 61 ACAGGATCTAGTTCGCGAAGTATACCGGTAGACCTTTCGTAGAGATGACAGTAATC 120  
DB 61 ACAGGATCTAGTTCGCGAAGTATACCGGTAGACCTTTCGTAGAGATGACAGTAATC 120  
QY 121 CCGAAATATATACATGACTGAAGGAGGAGTCTGTCATTCCCTGCGGGTACGTCA 180  
DB 121 CCGAAATATATACATGACTGAAGGAGGAGTCTGTCATTCCCTGCGGGTACGTCA 180  
QY 181 CTTAATCATCATCTGTTACTTTAAAGTTTCCACTTGAACCTTTCCTGATGGAATA 240  
DB 181 CTTAATCATCATCTGTTACTTTAAAGTTTCCACTTGAACCTTTCCTGATGGAATA 240  
QY 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAGAATA 300  
DB 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAGAATA 300  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTACA 360  
DB 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTACA 360  
QY 361 CATGACAAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATGGAATGAACTA 420  
DB 361 CATGACAAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATGGAATGAACTA 420  
QY 421 TCTGTTGAGAAAGCTTGTCTTAATTTGTACAGCAAGACTGAACTAAATGTGGGATT 480  
DB 421 TCTGTTGAGAAAGCTTGTCTTAATTTGTACAGCAAGACTGAACTAAATGTGGGATT 480  
QY 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTGTAAACCGGAC 540  
DB 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTGTAAACCGGAC 540  
QY 541 CTTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600  
DB 541 CTTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600  
QY 601 GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660  
DB 601 GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660

QY 661 AAGAACAGCACAATTTGTTCAGGGTCCATGAAAGGACAAAACCTCACACATGCCACCGTGC 720  
DB 661 AAGAACAGCACAATTTGTTCAGGGTCCATGAAAGGACAAAACCTCACACATGCCACCGTGC 720  
QY 721 CCAGCACCTGAACTCTTGGGGGACCGGTACGTCTTCTTCTTCCCCCAAAACCCCAAGGAC 780  
DB 721 CCAGCACCTGAACTCTTGGGGGACCGGTACGTCTTCTTCTTCCCCCAAAACCCCAAGGAC 780  
QY 781 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCACGAA 840  
DB 781 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCACGAA 840  
QY 841 GACCTCTGAGGTCAAGTTCNACTGGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACA 900  
DB 841 GACCTCTGAGGTCAAGTTCNACTGGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACA 900  
QY 901 AAGCCGGGGAGGAGAGTACAAACAGACGCTACCGTGTGGTTCAGCGTCTCACCGTCTG 960  
DB 901 AAGCCGGGGAGGAGAGTACAAACAGACGCTACCGTGTGGTTCAGCGTCTCACCGTCTG 960  
QY 961 CACCAGGACTGGCTGAAATGGCAAGGAGTACAAAGTGCAGAGTCTCCACAAAGCCCTCCCA 1020  
DB 961 CACCAGGACTGGCTGAAATGGCAAGGAGTACAAAGTGCAGAGTCTCCACAAAGCCCTCCCA 1020  
QY 1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1080  
DB 1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1080  
QY 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTTCAGCTGCTGCTGTC 1140  
DB 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTTCAGCTGCTGCTGTC 1140  
QY 1141 AAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGAGCAATGGGACCCGGAGAAC 1200  
DB 1141 AAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGAGCAATGGGACCCGGAGAAC 1200  
QY 1201 AACTTACAGACACCGCTCCCGTCTGGACTCCGACCGCTCTTCTTCTCTACAGCAAG 1260  
DB 1201 AACTTACAGACACCGCTCCCGTCTGGACTCCGACCGCTCTTCTTCTCTACAGCAAG 1260  
QY 1261 CTCAACCTGGACAAAGAGAGAGTGGCAGCAGGGGAACTGTTCTCATGCTCCGTGATGAT 1320  
DB 1261 CTCAACCTGGACAAAGAGAGAGTGGCAGCAGGGGAACTGTTCTCATGCTCCGTGATGAT 1320  
QY 1321 GAGGCTCTGCACACCACTACACGACAGAGAGCTCTCCCTGCTCCGGGTAAATGA 1377  
DB 1321 GAGGCTCTGCACACCACTACACGACAGAGAGCTCTCCCTGCTCCGGGTAAATGA 1377

RESULT 3

AAA91074

ID AAA91074 standard; DNA; 1453 BP.

XX

AC AAA91074;

XX

DT 05-APR-2001 (first entry)

XX

DE Flt1 receptor fusion protein Flt1D2, Flk1D3, FcDeltaC1(a) coding sequence.

XX

KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

XX

KW plasma leakage; vascular permeability; IgG Fc region; ss.

XX

OS Unidentified.

XX

FN WO200075319-A1.

XX

PD 14-DEC-2000.

XX

PF 23-MAY-2000; 2000WO-US014142.

XX

PR 08-JUN-1999; 99US-0138133P.

XX



FH Key Location/Qualifiers  
 FT CDS 69..1445  
 FT /\*tag= a  
 FT /product= "FltID2.FlkID3.FcDELTAcl(a)"  
 FX  
 FN WO200260489-A1.  
 XX 08-AUG-2002.  
 XX 28-JAN-2002; 2002WO-US002466.  
 XX 31-JAN-2001; 2001US-00773877.  
 PR (REG-) REGENERON PHARM INC.  
 PA Xia Y, Rudge JS, Yancopoulos GD;  
 XX WPI; 2002-608488/65.  
 DR P-PSDB; ABP52447.  
 XX  
 PT Treating psoriasis and enhancing wound healing in humans comprises the  
 PT administration of a vascular endothelial cell growth factor (VEGF)  
 PT antagonist.  
 PS Example 17; Fig 21A-C; 179pp; English.  
 XX The present invention describes a method for treating psoriasis and  
 CC enhancing wound healing in a mammal or a human. The method comprises  
 CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
 CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
 CC antiinflammatory, vulnary, antiasthmatic, antirheumatic, antiarthritic,  
 CC nephrotropic and ophthalmological activities. The method can be used in  
 CC treating psoriasis and enhancing wound healing in humans by administering  
 CC VEGF antagonist. The method is also useful in treating clinical  
 CC conditions characterised by vascular permeability, oedema or  
 CC inflammation, such as brain oedema associated with injury, oedema  
 CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
 CC asthma, burns, kidney diseases, or eye disorders such as age-related  
 CC macular degeneration and diabetic retinopathy. The method may also be  
 CC used in making the polypeptide to decrease or inhibit plasma leakage and  
 CC or vascular permeability. The present sequence encodes  
 CC FltID2.FlkID3.FcDELTAcl(a) which is used in an example from the present  
 CC invention  
 XX  
 SQ Sequence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;  
 Query Match 96.5%; Score 1328.4; DB 6; Length 1453;  
 Best Local Similarity 98.6%; Pred. No. 3e-312;  
 Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;  
 1 ATGGTCAGCTACTGGGACACCGGGTCTCTGTGGCGCTGCTCAGCTGCTGCTTC 60  
 69 ATGGTCAGCTACTGGGACACCGGGTCTCTGTGGCGCTGCTCAGCTGCTGCTTC 128  
 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120  
 129 ACAGGATCTAGTTCGGG- - - - -GCTAGACCTTTCTGTAGAGATGTACAGTGAATC 179  
 121 CCGGAATATATACATGACTGAAGGAGGAGTCTGTATTCCTGCGGGTTCAGTCA 180  
 180 CCGGAATATATACATGACTGAAGGAGGAGTCTGTATTCCTGCGGGTTCAGTCA 239  
 181 CCTAACATCACTGTACTTTAAAGAGTTTCCACTTGACATTTGATCCCTGATGGAAA 240  
 240 CCTAACATCACTGTACTTTAAAGAGTTTCCACTTGACATTTGATCCCTGATGGAAA 299  
 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACAAAGAAATA 300  
 300 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACAAAGAAATA 359  
 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTACA 360  
 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTACA 419

QY 361 CATCGACAAACCAATACAATCATAGATGTGTCTTCTGAGTCCGTCTCATGGAATTGAACCTA 420  
 DB 420 CATCGACAAACCAATACAATCATAGATGTGTCTTCTGAGTCCGTCTCATGGAATTGAACCTA 479  
 QY 421 TCTGTGGAGAAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACCTAAATGTGGGGATT 480  
 DB 480 TCTGTGGAGAAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACCTAAATGTGGGGATT 539  
 QY 481 GACTTCAACTGGGAATATACCTTCTTCGAAGCATCAGCATAGAAGAACTTGTAAACCGAGAC 540  
 DB 540 GACTTCAACTGGGAATATACCTTCTTCGAAGCATCAGCATAGAAGAACTTGTAAACCGAGAC 599  
 QY 541 CTAAAAACCCAGTCTGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACCTATAGATGGT 600  
 DB 600 CTAAAAACCCAGTCTGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACCTATAGATGGT 659  
 QY 601 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
 DB 660 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719  
 QY 661 AAGAACAGCACATTTGTTCAGGCTCCATGAAAG- - - - -GACAAAACTCACACATGC 711  
 DB 720 AAGAACAGCACATTTGTTCAGGCTCCATGAAAGGGCCCGGGCGACAAAACTCACACATGC 779  
 QY 712 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAA 771  
 DB 780 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAA 839  
 QY 772 CCCAAGGACACCCCTCATGATCTCCCGGACCCCTCAGGTCACATCGTGGTGGTGGACGTG 831  
 DB 840 CCCAAGGACACCCCTCATGATCTCCCGGACCCCTCAGGTCACATCGTGGTGGTGGACGTG 899  
 QY 832 AGCCACAAAGACCCCTGAGGTCAGTTCACTGTGTAAGTACGTGACGGCGGTGGAGTGCATAT 891  
 DB 900 AGCCACAAAGACCCCTGAGGTCAGTTCACTGTGTAAGTACGTGACGGCGGTGGAGTGCATAT 959  
 QY 892 GCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGCTACCGTGTGGTGGTGGTGGTGGT 951  
 DB 960 GCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGCTACCGTGTGGTGGTGGTGGTGGT 1019  
 QY 952 ACCGTCTCTGACCAAGGATCGGTGTAATGGCAAGAGGTACAAAGTCAAGGTCTCAACAAA 1011  
 DB 1020 ACCGTCTCTGACCAAGGATCGGTGTAATGGCAAGAGGTACAAAGTCAAGGTCTCAACAAA 1079  
 QY 1012 GCCCTCCCGAGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCA 1071  
 DB 1080 GCCCTCCCGAGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCA 1139  
 QY 1072 CAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGGAGCAATGGG 1131  
 DB 1140 CAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGGAGCAATGGG 1199  
 QY 1132 TGCCTGTCAAAGGCTTTCTATCCCGAGCAGCATCCCGTGGAGTGGGAGAGCAATGGGAG 1191  
 DB 1200 TGCCTGTCAAAGGCTTTCTATCCCGAGCAGCATCCCGTGGAGTGGGAGAGCAATGGGAG 1259  
 QY 1192 CCGGAGAACAACTAAGACCAAGCTCCCGTGGTGGAGTCCCGAGCGGTCTTCTTCTCTC 1251  
 DB 1260 CCGGAGAACAACTAAGACCAAGCTCCCGTGGTGGAGTCCCGAGCGGTCTTCTTCTCTC 1319  
 QY 1252 TACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGGAGGAGGAGCAATGGGAGCAATGGG 1311  
 DB 1320 TATAGCAGCTCACCGTGGACAAAGAGCAGGTGGGAGGAGGAGCAATGGGAGCAATGGG 1379  
 QY 1312 GTGATGATGAGGCTGTGCAACAACTACACGAGAGAGGCTCTCCCTGTCTCCGGGT 1371  
 DB 1380 GTGATGATGAGGCTGTGCAACAACTACACGAGAGAGGCTCTCCCTGTCTCCGGGT 1439  
 QY 1372 AATGA 1377  
 DB 1440 AATGA 1445

```
RESULT 5
ID AAA91075 standard; DNA; 1444 BP.
AC AAA91075;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Flt1D2.VEGFR3D3.fcDeltaC1(a) DNA sequence.
XX
KW Flt1 receptor; fusion protein; chimeric protein; phamacokinetic;
XX plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REG-1) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI; 2001-071076/08.
XX
OR P-PSDB; AAY97595.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems.
XX
PS Claim 9; Fig 22; 159pp; English.
XX
CC This sequence encodes a fusion protein of the invention between the Flt1
CC receptor and the Fc region of IgG. The specification relates to modified
CC chimeric polypeptides with improved pharmacokinetics. The modified
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC been modified to improve their pharmacokinetic profile. The polypeptides
CC can be used to decrease or inhibit plasma leakage and/or vascular
CC permeability in a mammal
XX
SQ Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;

Query Match 76.2%; Score 1049.2; DB 5; Length 1444;
Best Local Similarity 86.7%; Pred No. 1.8e-244;
Matches 1201; Conservative 0; Mismatches 159; Indels 27; Gaps 3;

Qy 1 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGTCTCAGCTGCTCTCTC 60
Db 69 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGTCTCAGCTGCTCTCTC 128
Qy 61 ACAGATCTAGTTCGGGAAGTATACCGGTAGACCTTCGTAGAGATGACAGTGAATC 120
Db 129 ACAGATCTAGTTCGGGAAGTATACCGGTAGACCTTCGTAGAGATGACAGTGAATC 179
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Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACCTTTGATCCCTGATGGAAAA 240
Db 240 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACCTTTGATCCCTGATGGAAAA 299
Qy 241 GGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAAGTCAAAAGAAATA 300
Db 300 GGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAAGTCAAAAGAAATA 359
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360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 419
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Db 420 CATCGACAAACCAATACAATCATAGATGTGTTGTGATCCGTCTCATGGAATGAACTA 479
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAATTTGACAGCAAGAACTGAACTAAATGTGGGAT 480
Db 480 CTGCTAGGGGAGAGCTGGTCTCACTGACCGTGTGGGCTGAGTTTAACTCAGGTGTC 539
Qy 481 GACTTCAACTGGGAATACCTCTTCTTGAAGCATCAGCATAAAGAACTTTGTAACCGAGAC 540
Db 540 ACTTTGACTGGGACTACCCAGGAGCAGCAGCGGGGTAAAGTGGGTGCCGAGCGA 599
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGACCTTTAACTATAGATGGT 600
Db 600 CGCTCCCAACAGACCCACACAG-----AACTCTCCAGCATCTCTGACCATCAAC 650
Qy 601 GTAAACCCGAGTGACCAAGGATTTGTACCTGTGACAGATCCAGTGGGCTGATGACCAAG 660
Db 651 GTACGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACACGCGCATCCAGCGATTT 710
Qy 661 AAGAAACAGCACATTTGTGAGGTCCATGAAAA-----GGACAAAACTCACACATGC 711
Db 711 CGGAGAGACCGAGGTCAATTGTGATGAAATATGGCCCGGCGACAAACTCACACATGC 770
Qy 712 CCACCGTGCACGACCTGAACTCTCGGGGGAGCCGTGACGTCTTCTTCTTCCCTCCCAAAA 771
Db 771 CCACCGTGCACGACCTGAACTCTCGGGGGAGCCGTGACGTCTTCTTCTTCCCTCCCAAAA 830
Qy 772 CCCNAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTGCTGCTGCTGGGAGGTG 831
Db 831 CCCNAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTGCTGCTGCTGGGAGGTG 890
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Qy 892 GCCAAGACAAAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGTCTC 951
Db 951 GCCAAGACAAAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGTCTC 1010
Qy 952 ACCGTCTCTGACCAAGGACTCGCTGAATGCGCAAGGAGTACAAGTGCAGAGTCTCCAA 1011
Db 1011 ACCGTCTCTGACCAAGGACTCGCTGAATGCGCAAGGAGTACAAGTGCAGAGTCTCCAA 1070
Qy 1012 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCA 1071
Db 1071 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCA 1130
Qy 1072 CAGGTGTACACCTTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTTCAGCTGACC 1131
Db 1131 CAGGTGTACACCTTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTTCAGCTGACC 1190
Qy 1132 TGCTGTGTCAAGAGCTTCTATCCCGAGCATCGCTCCGTGTGGACTCCCGAGCGCTCCCTT 1191
Db 1191 TGCTGTGTCAAGAGCTTCTATCCCGAGCATCGCTCCGTGTGGACTCCCGAGCGCTCCCTT 1250
Qy 1192 CCGGAGAACAACTACAAAGACACGCTCTCCGTGTGGACTCCCGAGCGCTCCCTTCTCTC 1251
Db 1251 CCGGAGAACAACTACAAAGACACGCTCTCCGTGTGGACTCCCGAGCGCTCCCTTCTCTC 1310
Qy 1252 TACAGCAAGCTCACCGTGGACAAGAGAGAGGTGGCAGCAGGGGAAACGTCTTCTCATGTCC 1311
Db 1311 TATAGCAAGCTCACCGTGGACAAGAGAGAGGTGGCAGCAGGGGAAACGTCTTCTCATGTCC 1370
Qy 1312 GTGATGATGAGGCTCTGCAACCACTACACGAGAGAGCGCTCTCCCTGTCTCCGGGT 1371
Db 1371 GTGATGATGAGGCTCTGCAACCACTACACGAGAGAGCGCTCTCCCTGTCTCCGGGT 1430
Qy 1372 AAATGA 1377
|||
```







Db 943 CACCGAGTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCAACAAAGCCCTCCCA 1002  
 Qy 1021 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCACAGGTGTAC 1080  
 Db 1003 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCACAGGTGTAC 1062  
 Qy 1081 ACCCTGCCCCATCCCGGATGAGTGCACCAAGAACCCAGGTGAGCTGACCTGCTGCTGTC 1140  
 Db 1063 ACCCTGCCCCATCCCGGATGAGTGCACCAAGAACCCAGGTGAGCTGACCTGCTGCTGTC 1122  
 Qy 1141 AAAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGAAC 1200  
 Db 1123 AAAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGAAC 1182  
 Qy 1201 AACTACAAGACCAAGCCCTCCCGTGGTGGACTCCGAGCGCTCTCTCTCTACAGCAAG 1260  
 Db 1193 AACTACAAGACCAAGCCCTCCCGTGGTGGACTCCGAGCGCTCTCTCTCTACAGCAAG 1242  
 Qy 1261 CTCACCGTGGACCAAGCAGGAGTGGCAGCAGGAGAAAGTCTTCTCATGCTCCGATGATCAT 1320  
 Db 1243 CTCACCGTGGACCAAGCAGGAGTGGCAGCAGGAGAAAGTCTTCTCATGCTCCGATGATCAT 1302  
 Qy 1321 GAGGCTTCGACCAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1377  
 Db 1303 GAGGCTTCGACCAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1359

## RESULT 8

ABQ74605

ID ABQ74605 standard; cDNA; 1359 BP.

XX AC ABQ74605;

XX DT 23-OCT-2002 (first entry)

XX DE Mutation 2 Flt1(2-3 delta B)-Fc nucleotide sequence.  
 XX Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
 KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
 KW vulnery; antiaesthetic; antirheumatic; antiarthritic; nephrotropic;  
 KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
 KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
 KW kidney disease; eye disorder; age-related macular degeneration;  
 KW diabetic retinopathy; gene; ss.  
 XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 XX CDS 1..1359  
 XX /\*tag= a  
 XX /product= "Mut2:Flt1(2-3 delta B)-Fc protein"  
 XX WO200260489-A1.  
 XX 08-AUG-2002.  
 XX 28-JAN-2002; 2002WO-US002466.  
 XX 31-JAN-2001; 2001US-00773877.  
 XX (REG- ) REGENERON PHARM INC.  
 XX Xia Y, Rudge JS, Yancopoulos GD;  
 XX WPI; 2002-608488/65.  
 XX P-PSDB; ABP52444.  
 XX Treating psoriasis and enhancing wound healing in humans comprises the  
 PT administration of a vascular endothelial cell growth factor (VEGF)  
 PT antagonist.

## Example 12; Fig 14A-C; 179pp; English.

PS The present invention describes a method for treating psoriasis and  
 XX enhancing wound healing in a mammal or a human. The method comprises  
 CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
 CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
 CC antiinflammatory, vulnery, antiaesthetic, antirheumatic, antiarthritic,  
 CC nephrotropic and ophthalmological activities. The method can be used in  
 CC treating psoriasis and enhancing wound healing in humans by administering  
 CC VEGF antagonist. The method is also useful in treating clinical  
 CC conditions characterised by vascular permeability, oedema or  
 CC inflammation, such as brain oedema associated with injury, oedema  
 CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
 CC asthma, burns, kidney diseases, or eye disorders such as age-related  
 CC macular degeneration and diabetic retinopathy. The method may also be  
 CC used in making the polypeptide to decrease or inhibit plasma leakage and  
 CC or vascular permeability. The present sequence encodes Mut2:Flt1(2-3  
 CC delta B)-Fc which is used in an example from the present invention  
 XX

SQ Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 6; Length 1359;

Best Local Similarity 86.3%; Pred. No. 5.3e-242;

Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

Qy 1 ATGGTCAAGTACTGGGACACCGGGGTCTGCTGTGCGCGTCTGCTCAGCTGTCTGCTCTC 60  
 Db 1 ATGGTCAAGTACTGGGACACCGGGGTCTGCTGTGCGCGTCTGCTCAGCTGTCTGCTCTC 60  
 Qy 61 ACAGGATCTAGTCTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120  
 Db 61 ACAGGATCTAGTCTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111  
 Qy 121 CCCGAAATTTACACATGACTGAAGGAAGGGAGTCTGTCATTTCCCTGCGCGGTACGTCA 180  
 Db 112 CCCGAAATTTACACATGACTGAAGGAAGGGAGTCTGTCATTTCCCTGCGCGGTACGTCA 171  
 Qy 181 CCTAACATCACTGTACTTTTAAAGAGTTTCCACTTCACACTTTTGATCCCTGATGGAAA 240  
 Db 172 CCTAACATCACTGTACTTTTAAAGAGTTTCCACTTCACACTTTTGATCCCTGATGGAAA 231  
 Qy 241 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAAGCTGCAAAAGAAATA 300  
 Db 232 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAAGCTGCAAAAGAAATA 291  
 Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 360  
 Db 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 351  
 Qy 361 CATCGACAAACCAATACAATCATAGATGTGTTCTGAGTCGCTCTCATGGAATTTGAACATA 420  
 Db 352 CATCGACAAACCAATACAATCATAGATGTGTTCTGAGTCGCTCTCATGGAATTTGAACATA 411  
 Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATT 480  
 Db 412 CTTAGAGGCCATCTCTTTGCTCAATTTGTACTGCTACCACTCCCTTTGAACACGAGAGTT 471  
 Qy 481 GACTTCAACTGGGAAATACCTTCTTGAAGCATCAGCATTAAGAACTTTGTAACCCGAGAC 540  
 Db 472 CAAATGACCTGGAGTTTACCCCTGATGAAATTTGACCAAGCAATTTCCCATGCGCAATATTC 531  
 Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTGAGCACCTTAACTATAGATGGT 600  
 Db 532 TACAGTGTCTTACTATTGACAAATGCAAGCAAGAGCACTTTATCTTGTGCT 591  
 Qy 601 GTAAACCGGAGTGACCAAGGATTGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660  
 Db 592 GTAAACCGGAGTGACCAAGGATTGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 642  
 Qy 661 AAGAACAGCAGCATTTGTGCGGTCATGAAAGCAAAACTCACAACATGCCCAACCGTGC 720  
 Db 643 GATAAAGCAGCGCGCGGCGAGCCCAATCTTGTGACAAAACTCACAACATGCCCAACCGTGC 702



Db 646 TCTGTTAAACATCTCAGTGCATATATATGATAAAGCAGGCCCCGGGAGCCCCAAATCTTGT 705  
Qy 694 GACAAAACCTCACATGCCCCACCGTCCAGCAGCACCTGAACTCCTCGGGGGACCGTCAGTC 753  
Db 706 GACAAAACCTCACATGCCCCACCGTCCAGCAGCACCTGAACTCCTCGGGGGACCGTCAGTC 765  
Qy 754 TTCCTCTTCCCCCCCCAAAGCAGCACCTCTCATGATCTCCCGGAGCCCTTGAGGTACACA 813  
Db 766 TTCCTCTTCCCCCCCCAAAGCAGCACCTCTCATGATCTCCCGGAGCCCTTGAGGTACACA 825  
Qy 814 TCGTGTGGTGGAGCTGAGGACACGAGACCTCTGAGGTCAAGTTCAACTGTGTAAGTGGAC 873  
Db 826 TCGTGTGGTGGAGCTGAGGACACGAGACCTCTGAGGTCAAGTTCAACTGTGTAAGTGGAC 885  
Qy 874 GCGGTGGAGGTGCATAAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACAAGCAGCAGTAC 933  
Db 886 GCGGTGGAGGTGCATAAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACAAGCAGCAGTAC 945  
Qy 934 COTGTGGTCAAGCTCTCACCGTCTCTGCACAGGACTGGCTGAAATGGCAAGGAGTACAAAG 993  
Db 946 COTGTGGTCAAGCTCTCACCGTCTCTGCACAGGACTGGCTGAAATGGCAAGGAGTACAAAG 1005  
Qy 994 TCCAAAGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
Db 1006 TCCAAAGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 1065  
Qy 1054 GGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTACACCAAG 1113  
Db 1066 GGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTACACCAAG 1125  
Qy 1114 AACCAAGTCAAGCTGCTGCTGCTCAAGAGCTTCTATCCAGCAGCATCGCCGTGGAG 1173  
Db 1126 AACCAAGTCAAGCTGCTGCTGCTCAAGAGCTTCTATCCAGCAGCATCGCCGTGGAG 1185  
Qy 1174 TGGGAGACCAATGGCAGCCGAGAACAACTACAAAGACACGCTTCCCGTGTGAGTCC 1233  
Db 1186 TGGGAGACCAATGGCAGCCGAGAACAACTACAAAGACACGCTTCCCGTGTGAGTCC 1245  
Qy 1234 GAGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGCAGCAGGGG 1293  
Db 1246 GAGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGCAGCAGGGG 1305  
Qy 1294 AACGCTTCTCATGTCCCGTATCATGAGGCTCTGCACAAACCACTACACGAGAAGAGC 1353  
Db 1306 AACGCTTCTCATGTCCCGTATCATGAGGCTCTGCACAAACCACTACACGAGAAGAGC 1365  
Qy 1354 CTCTCCCTGTCTCCGGGTAATGA 1377  
Db 1366 CTCTCCCTGTCTCCGGGTAATGA 1389

RESULT 10  
ABQ74606  
ID ABQ74606 standard; cDNA; 1389 BP.  
XX  
AC ABQ74606;  
XX  
DT 23-OCT-2002 (first entry)  
XX  
DE Mutation 3 Flt1(2-3)-Fc nucleotide sequence.  
XX  
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnary; antiaesthetic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
CDS 1..1389  
/\*tag= a  
/product= "Mut3:Flt1(2-3)-Fc protein"  
FN WO200260489-A1.  
PD 08-AUG-2002.  
PF 28-JAN-2002; 2002WO-US002466.  
PR 31-JAN-2001; 2001US-00773877.  
PA (REGG-) REGENERON PHARM INC.  
PI Xia Y, Rudge JS, Yancopoulos GD;  
XX WPI; 2002-608488/65.  
DR  
XX  
PT Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.  
XX  
PS Example 13; Fig 15A-C; 179pp; English.  
XX  
CC The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnary, antiaesthetic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes Mut3:Flt1(2-3)-Fc  
CC which is used in an example from the present invention  
XX  
SQ Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;  
Query Match 75.08; Score 1032.4; DB 6; Length 1389;  
Best Local Similarity 85.58; Pred. No. 2.2e-240;  
Matches 1201; Conservative 0; Mismatches 161; Indels 42; Gaps 3;  
Qy 1 ATGCTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
Db 1 ATGCTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCGGAAAGTGATACCGGTAGACCTTTCTGTPAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCGGAAAGTGATACCGGTAGACCTTTCTGTPAGAGATGTACAGTGAATC 111  
Qy 121 CCGGAAATATACATGATGCTGAGGAGGAGGAGTCTGCTATTCCTCCGCGGTACGTCAC 180  
Db 112 CCGGAAATATACATGATGCTGAGGAGGAGGAGTCTGCTATTCCTCCGCGGTACGTCAC 171  
Qy 181 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTTCGACACTTTTGATCCCTGATGGAAAA 240  
Db 172 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTTCGACACTTTTGATCCCTGATGGAAAA 231  
Qy 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTGAAGGAAATA 300  
Db 232 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTGAAGGAAATA 291  
Qy 301 GGGCTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 360  
Db 292 GGGCTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 351  
Qy 361 CATCGACAAACCAATAACAATCATAGATGTGTTCTGAGTCCGTCTCATGGAATGAACTA 420

[illegible]

AAA91070	AAA91070 standard; DNA; 1674 BP.
XX	XX
XX	XX
AC	AAA91070;
XX	XX
DT	05-APR-2001 (first entry)
XX	XX
DE	Flt1 receptor fusion protein Mut1:Flt1(1-3deltaB)-Fc coding sequence.
XX	XX
KW	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW	plasma leakage; vascular permeability; IgG Fc region; ss.
XX	XX
OS	Unidentified.
XX	XX
FH	Key Location/Qualifiers
FT	CDS 1..1674
FT	/*tag= a
FT	/product= "Flt1(1-3deltaB)-Fc"
XX	XX
PN	WO200075319-A1.
XX	XX
PD	14-DEC-2000.
XX	XX
FF	23-MAY-2000; 2000WO-US014142.
XX	XX
PR	08-JUN-1999; 99US-0138133P.
XX	XX
PA	(REGG-) REGENERON PHARM INC.
XX	XX
PI	Papadopoulos NJ, Davis S, Yancopoulos GD;
XX	XX
DR	WPI; 2001-071076/08.
DR	P-PSDB; AAY97590.
XX	XX
PT	Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT	and its fragments, useful for diagnosis, evaluation, and treatment of
PT	diseases associated with the gene expression and for producing model
PT	systems.
XX	XX
PS	Claim 9; Fig 13; 159pp; English.
XX	XX
CC	This sequence encodes a fusion protein of the invention between the Flt1
CC	receptor and the Fc region of IgG. The specification relates to modified
CC	chimeric polypeptides with improved pharmacokinetics. The modified
CC	chimeric polypeptides are preferably Flt1 receptor polypeptides that have
CC	been modified to improve their pharmacokinetic profile. The polypeptides
CC	can be used to decrease or inhibit plasma leakage and/or vascular
CC	permeability in a mammal
XX	XX
SQ	Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;
Query Match	71.7%; Score 987.4; DB 5; Length 1674;
Best Local Similarity	86.1%; Pred. No. 1.9e-229;
Matches 1119; Conservative	0; Mismatches 171; Indels 9; Gaps 2;
QY	79 AGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATCCCGGAAATATATACATG 138
Db	
385 AGTGATACAGGTAGACCTTTTCGTAGAGATGTACAGTGAATCCCGGAAATATATACATG 444	
QY	139 ACTGAAGGAGGGAGCTCGTCATTCCTCGCGGGTTACGTCACTTAACATCACTGTACT 198
Db	
445 ACTGAAGGAGGGAGCTCGTCATTCCTCGCGGGTTACGTCACTTAACATCACTGTACT 504	
QY	199 TTAATAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACGCATATCTGGACAGT 258
Db	
505 TTAATAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACGCATATCTGGACAGT 564	
QY	259 AGAAGGGCTTCATCATATCAATGCAACGTFACAAAGAAATAGGGCTTCTGACCTGTCAA 318
Db	
565 AGAAGGGCTTCATCATATCAATGCAACGTFACAAAGAAATAGGGCTTCTGACCTGTCAA 624	
QY	319 GCAACAGTCAATGGGCACTTTGTATAAGCAAACTATCTCACATCGCAAAACCAATACA 378

Db 625 GCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACACATCGACAAACCAATACA 684  
QY 379 ATCTAGATAGTGTCTGAGTCCGCTCATGGAATTTGAATCTATCTGTTGGAGAAAGCTT 438  
Db 685 ATCTAGATAGTCAATAAGACACACGCCCGCTCAAAATTTACTTTAGAGGCCATCTCTT 744  
QY 439 GTCTTAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCAATTTGTACTTACCCTCCCTTGAACACGAGAGTTCAAAATGACCTGGAGTTAC 804  
QY 499 CTTCTTTCGACATCAGATCAAGAACTTGTAAACCGAGACTTAAACCCAGCTGCTGG 558  
Db 805 CTTGATGAATTTGACCAAGCAATTTCCCATGCGCAACATATTTACAGATGTTCTTCTATT 864  
QY 559 AGTGAGATGAAGAAATTTTGTAGACCTTTAACTATAGATGGTGTAAACCGGAGTCAACAA 618  
Db 865 GACAAATGACAGACAAAGACAAAGGACTTTTATCTTGTCTGTAA---GGAGTGACCA 921  
QY 619 GGATTTGACCTGTGACAGCTCCAGTGGGCTGATGACCAAGAAAGACGACATTTGTC 678  
Db 922 TCATTTCAATCTGTTAAACACCTC-----AGTGCATATATATGATAAAGCAGGCCCGGC 975  
QY 679 AGGTGTCATGAAGAGCAAACTACACATCCACCGTCCAGCAGCTGAATCTCTG 738  
Db 976 GAGCCCAATCTTGTGACAAACTCACACATCCACCGTCCAGCAGCTGAATCTCTG 1035  
QY 739 GGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCG 798  
Db 1036 GGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCG 1095  
QY 799 ACCCTGAGGTCACTGCTGTGTGGTGGACGACGACCAAGACCCCTGAGGTCAAGTTC 858  
Db 1096 ACCCTGAGGTCACTGCTGTGTGGTGGACGACGACCAAGACCCCTGAGGTCAAGTTC 1155  
QY 859 AACTGTTAGTGGACGGGCTGAGGTGCATATATGCAAGAAAGCCCGGAGAGCAG 918  
Db 1156 AACTGTTAGTGGACGGGCTGAGGTGCATATATGCAAGAAAGCCCGGAGAGCAG 1215  
QY 919 TACACAGCAGTACCGTGTGTGCTGAGCTCTCAGCGTCTGACACGAGCTGCTGAT 978  
Db 1216 TACACAGCAGTACCGTGTGTGCTGAGCTCTCAGCGTCTGACACGAGCTGCTGAT 1275  
QY 979 GGCAGGAGTACAGTGCAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACC 1038  
Db 1276 GGCAGGAGTACAGTGCAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACC 1335  
QY 1039 ATCTCAAGCCAAAGGAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATCCCGG 1098  
Db 1336 ATCTCAAGCCAAAGGAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATCCCGG 1395  
QY 1099 GATGAGCTGACCAAGAACAGCTGAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGC 1158  
Db 1396 GATGAGCTGACCAAGAACAGCTGAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGC 1455  
QY 1159 GACATCGCGTGGAGAGCAATGGGAGCCGAGCAAACTCAAGACCAAGCCT 1218  
Db 1456 GACATCGCGTGGAGAGCAATGGGAGCCGAGCAAACTCAAGACCAAGCCT 1515  
QY 1219 CCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGC 1278  
Db 1516 CCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGC 1575  
QY 1279 AGTGGCAGCAGGGAAGCTCTTCTTCTTCTTCTGATGATGAGGCTCTGCAACACAC 1338  
Db 1576 AGTGGCAGCAGGGAAGCTCTTCTTCTTCTTCTGATGATGAGGCTCTGCAACACAC 1635  
QY 1339 TACAGCAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1377  
Db 1636 TACAGCAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1674

RESULT 12  
ABQ74604

ID ABQ74604 standard; cDNA; 1674 BP.  
XX AC ABQ74604;  
XX DT 23-OCT-2002 (first entry)  
XX DE Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence.  
XX KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
XX KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
XX KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
XX KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
XX KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
XX KW kidney disease; eye disorder; age-related macular degeneration;  
XX KW diabetic retinopathy; gene; ss.  
XX OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
CDS 1..1674  
/\*tag= a  
/product= "Mut1:Flt1(1-3 delta B)-Fc protein"

WO200260489-A1.

08-AUG-2002.

28-JAN-2002; 2002MO-US002466.

31-JAN-2001; 2001US-00773877.

(REGE-) REGENERON PHARM INC.

Xia Y, Rudge JS, Yancopoulos GD;

WPI; 2002-608488/65.

P-PSDB; ABP52443.

Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF) antagonist.

Example 11; Fig 13A-D; 179pp; English.

The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Mut1:Flt1(1-3 delta B)-Fc which is used in an example from the present invention

Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;

Query Match 71.7%; Score 987.4; DB 6; Length 1674;

Best Local Similarity 86.1%; Pred. No. 1.9e-229;

Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;

QY 79 AGTGATACCGGTAGACCTTTCTGATGAGATGTACAGTGAATCCCGAAATATACACATG 138

Db 385 AGTGATACCGGTAGACCTTTCTGATGAGATGTACAGTGAATCCCGAAATATACACATG 444

QY 139 ACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTAGCTCACCTAACATCACTGTTACT 198

Db 445 ACTGAAGGAGGAGCTCGTCACTTCCTGCGGGTTACGTCACTTAACATCACTGTTACT 504  
Qy 199 TTAATAAAGTTTCCACTTGGACACTTTGATCCCTGATGGAAGAAACGATTAATCTGGGACAGT 258  
Db 505 TTAATAAAGTTTCCACTTGGACACTTTGATCCCTGATGGAAGAAACGATTAATCTGGGACAGT 564  
Qy 259 AGAAGGGCTTCATCATATCAATCAAAATGAACGATCAAGAAATAGGCTTCTGACCTGTCAA 318  
Db 565 AGAAGGGCTTCATCATATCAAAATGAACGATCAAGAAATAGGCTTCTGACCTGTCAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGTGGTTCTGAGTCCGCTTCATAGGAATTTGAATCTATCTGTTGGAGAAAAGCTT 438  
Db 685 ATCATAGATGTCCAAATGAACACACACCGCCAGTCAAAATTAATTAGAGGCCATCTCTT 744  
Qy 439 GTCTTAATTTACAGCAAGAACTGAATAAATGTGGGATTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCAATTTGACTGTACCACTCCCTTGAACACGAGAGTTCAAATGACCTGGAGTTAC 804  
Qy 499 CTTCTTCCGAAGCATCAGCATAGAAGAACTGTAAACCGAGACCTTAAAAACCCAGTCTGGG 558  
Db 805 CTTGATGAATTTGACCAAGCAATTCCTCATGCCACATATTTCTACAGTGTCTTACTATT 864  
Qy 559 AGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGTGTAAACCGGAGTGACCAA 618  
Db 865 GACAAATGCAGAACAAAGACAAAGGACTTTATATCTGTCTGTGTAA--GGAGTGGACCA 921  
Qy 619 GGAATGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAGAAAGACAGACATTTGTC 678  
Db 922 TCATTCAAATCTGTTAACACCTC-----AGTGCATATATATGATAAAGCAGGCCCGGGC 975  
Qy 679 AGGATCCATGAAGAGCAAAACTCACATATGCCCGTCCCGACGACCTTGAATCTCTG 738  
Db 976 GAGCCCAATCTTTGACAAACTCACATATGCCCGTCCCGACGACCTTGAATCTCTG 1035  
Qy 739 GGGAGACCGTCAGTCTTCTTCCCGCCAAACCCCAAGGACACCTCATGATCTCCGG 798  
Db 1036 GGGGACCGTCAGTCTTCTTCCCGCCAAACCCCAAGGACACCTCATGATCTCCGG 1095  
Qy 799 ACCCTGAGGTCAATGCGTGGTGTGACGTGACGTGACGACGACGACCTTGAATCTCAAGTTC 858  
Db 1096 ACCCTGAGGTCAATGCGTGGTGTGACGTGACGACGACGACCTTGAATCTCAAGTTC 1155  
Qy 859 AACTGGTACGTGGCGGTGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAG 918  
Db 1156 AACTGGTACGTGGCGGTGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAG 1215  
Qy 919 TACACAGCATACCGTGTGTCAGCTCTCCCGTCTGACACGAGCTGCTGAAT 978  
Db 1216 TACACAGCATACCGTGTGTCAGCTCTCCCGTCTGACACGAGCTGCTGAAT 1275  
Qy 979 GGCAGAGGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCGCATCGAAGAAC 1038  
Db 1276 GGCAGAGGATCAAGTGAAGGTCTCCAAAGAGCCCTCCAGCCCGCATCGAAGAAC 1335  
Qy 1039 ATCTCCAAAGCCAAAGGCGACCCCGAGAACCCACAGGTGTACCCCTGCCCCATCCCGG 1098  
Db 1336 ATCTCCAAAGCCAAAGGCGACCCCGAGAACCCACAGGTGTACCCCTGCCCCATCCCGG 1395  
Qy 1099 GATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGC 1158  
Db 1396 GATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGC 1455  
Qy 1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAAACAATCAAGACCAAGCCT 1218  
Db 1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAAACAATCAAGACCAAGCCT 1515  
Qy 1219 CCGTGTCTGAGTCTCGAGCGCTCTTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278

Db 1516 CCGTGTCTGACTCCGAGCGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575  
Qy 1279 AGTGGCAGCAGAGGGAACGTCCTTCTCATGTCTCGTGTATGATGAGGCTCTGCAACAC 1338  
Db 1576 AGTGGCAGCAGAGGGAACGTCCTTCTCATGTCTCGTGTATGATGAGGCTCTGCAACAC 1635  
Qy 1339 TACACGCAAGAGCGCTCTCCCTGTCTCCGGTAAATGA 1377  
Db 1636 TACACGCAAGAGCGCTCTCCCTGTCTCCGGTAAATGA 1674  
RESULT 13  
AAA91073  
ID AAA91073 standard; DNA; 1704 BP.  
XX  
XX AAA91073;  
AC  
DT 05-APR-2001 (first entry)  
XX  
DE Flt1 receptor fusion protein Mut4:Flt1 (1-3R-N)-Fc coding sequence.  
XX  
XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
XX Unidentified.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1704  
FT /\*tag= a  
FT /product= "Flt1(1-3R-N)-Fc"  
XX  
XX WO200075319-A1.  
XX  
XX 14-DEC-2000.  
XX  
XX 23-MAY-2000; 2000WO-US014142.  
XX  
XX 08-JUN-1999; 99US-0138133P.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX WPI; 2001-071076/08.  
DR P-PSDB; AAY97593.  
XX  
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX Claim 9; Fig 16; 159pp; English.  
PS  
XX This sequence encodes a fusion protein of the invention between the Flt1  
CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
CC permeability in a mammal  
XX  
SQ Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;  
Query Match 71.3%; Score 982.4; DB 5; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 3.2e-228;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;  
Qy 79 AGTGATACCGGTAGACCTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACATG 138  
Db 385 AGTGATACCGGTAGACCTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACATG 444  
Qy 139 ACTGAGGAGGAGGAGCTCGTCACTTCCTGCGGGTACGTCACTTAACATCACTGTTACT 198

Db 445 ACTGAAGGAGGAGCTCGTCAATCCCTGCGGGTTACGTCACTAAACATCACTGTTACT 504  
Qy 199 TTAATAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAACGCGATAATCTGGACAGT 258  
Db 505 TTAATAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAACGCGATAATCTGGACAGT 564  
Qy 259 AGAAGGGCTTCATCATATCAAAATGCAAGTGAACAAAGAAATAGGCGTTCTGACCTGTGAA 318  
Db 565 AGAAGGGCTTCATCATATCAAAATGCAAGTGAACAAAGAAATAGGCGTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCATTTGATAGACAAACTATCTCACATCGACCAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCATTTGATAGACAAACTATCTCACATCGACCAACCAATACA 684  
Qy 379 ATCATAGATGTGGTTCTGAGTCCGCTCATGGAATGAACTATCTGTTGGAGAAAAGCTT 438  
Db 685 ATCATAGATGTCAATAAGACACACCGCCAGTCAAAATTAATTTAGAGGCCATCTTT 744  
Qy 439 GTCTTAAATTTGACAGCAAGAACTGAACTTAATATGTTGGGATTTGACTTCAACTTGGGAATAC 498  
Db 745 GTCTTCAATTTGACTGCTACCACTCCCTTGAACACGAGAGTTCAAAATGACCTGGAGTTAC 804  
Qy 499 CTTCTTTCGAGCATCAGCATGAAGAACTTTGTAACCGGACCTTAAACCCAGTCTGGG 558  
Db 805 CTTGATGAAAAAATAAGAACGCTTCCGTAAGCGACGAATGACCAAGCAATTC---- 860  
Qy 559 AGTGAGATGAAGAAATTTTGAGACCTTAACTATAGATGGTGTAAACCGGAGTGACCAA 618  
Db 861 --CCATGCCACATATTTCTAGTGTCTTACTATTGCAAAATGCAAGCAAAAGACAAA 918  
Qy 619 GAATGTTACCTGTGACAGATCCAGTGGGTGATGACCAAGAAAGACAGACATTTTCTC 678  
Db 919 GGACTTTATCTGTGCTGTAAGAGTGGACCATCATTTCAAATCTGTTAAACACCTCACTG 978  
Qy 679 AGGTCCTATGAAA-----GGACAAACTCACACATGC 711  
Db 979 CATATATATGATAAAGACGAGCCCGCGGAGCCCAAAATCTGTGACAAAACTCACACATGC 1038  
Qy 712 CCACCGTCCGACGACCTGAACTCTCTGGGGGACCGTCACTGCTTCTCTCCGCCCAAAA 771  
Db 1039 CCACCGTCCGACGACCTGAACTCTCTGGGGGACCGTCACTGCTTCTCTCTCCGCCCAAAA 1098  
Qy 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGACGTG 831  
Db 1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGACGTG 1158  
Qy 832 AGCCACGAGACCTTGAAGTCAAGTTCACTGTTAGTGGAGCGGTGGAGGTGCAATAT 891  
Db 1159 AGCCACGAGACCTTGAAGTCAAGTTCACTGTTAGTGGAGCGGTGGAGGTGCAATAT 1218  
Qy 892 GCCTAAGACAAAGCCCGGAGGAGCAGTACACAGCAGTACCGTGTGCTGAGGTCTCTC 951  
Db 1219 GCCTAAGACAAAGCCCGGAGGAGCAGTACACAGCAGTACCGTGTGCTGAGGTCTCTC 1278  
Qy 952 ACCGTCCTGCACAGGACTGGCTGAATGGCAGGAGTACAAGTCAAGTCTCCCAACAAA 1011  
Db 1279 ACCGTCCTGCACAGGACTGGCTGAATGGCAGGAGTACAAGTCAAGTCTCCCAACAAA 1338  
Qy 1012 GCGCTCCAGCGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA 1071  
Db 1339 GCGCTCCAGCGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA 1398  
Qy 1072 CAGGTGTACACCTCCCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTCAAGCTGACC 1131  
Db 1399 CAGGTGTACACCTCCCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTCAAGCTGACC 1458  
Qy 1132 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCGAG 1191  
Db 1459 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCGAG 1518  
Qy 1192 CCGGAGAACATACAGACACGCTCCCGTGTGAGCTCCGAGCGTCTCTTCTTCTC 1251  
Db 1519 CCGGAGAACATACAGACACGCTCCCGTGTGAGCTCCGAGCGTCTCTTCTTCTC 1578

Qy 1252 TACAGCAAGCTCACCGTGGACAAGACAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTCC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAAGACAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTCC 1638  
Qy 1312 GTGATGATGAGGCTCTGCAACAACATACACGAGAGAGCCTCTCCCTGTCTCCGGGT 1371  
Db 1639 GTGATGATGAGGCTCTGCAACAACATACACGAGAGAGCCTCTCCCTGTCTCCGGGT 1698  
Qy 1372 AAATGA 1377  
Db 1699 AAATGA 1704  
RESULT 14  
ABQ74607  
ID ABQ74607 standard; cDNA; 1704 BP.  
XX  
AC ABQ74607;  
XX  
DT 23-OCT-2002 (first entry)  
XX  
DE Mutation 4 Flt1(2-3 R-N)-Fc nucleotide sequence.  
XX  
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..1704  
FT /\*tag= a  
FT /product= "Mut4:Flt1(2-3 R-N)-Fc protein"  
XX  
PN WO200260489-A1.  
XX  
PD 08-AUG-2002.  
XX  
PF 28-JAN-2002; 2002WO-US002466.  
XX  
PR 31-JAN-2001; 2001US-00773877.  
XX  
PA (REG- ) REGENERON PHARM INC.  
XX  
PI Xia Y, Rudge JS, Yancopoulos GD;  
XX  
XX WPI; 2002-608489/65.  
DR P-ESDB; ABP52446.  
XX  
XX Treating psoriasis and enhancing wound healing in humans comprises the  
XX administration of a vascular endothelial cell growth factor (VEGF)  
XX antagonist.  
XX  
XX Example 14; Fig 16A-D; 179pp; English.  
XX  
XX The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
XX administering a vascular endothelial cell growth factor (VEGF) antagonist  
XX to the mammal or human. A VEGF antagonist has antipsoriatic,  
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
XX nephrotropic and ophthalmological activities. The method can be used in  
XX treating psoriasis and enhancing wound healing in humans by administering  
XX VEGF antagonist. The method is also useful in treating clinical  
XX conditions characterised by vascular permeability, oedema or  
XX inflammation, such as brain oedema associated with injury, oedema  
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),  
XX asthma, burns, kidney diseases, or eye disorders such as age-related



CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 R-  
XX >N)-Fc which is used in an example from the present invention  
SQ Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;

Query Match 71.3%; Score 982.4; DB 6; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 3.2e-228;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;

Qy 79 AGTGATACCGGTAGACCTTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACACATG 138  
Db |||||  
Qy 385 AGTGATACAGTAGACCTTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACACATG 444  
Db |||||

Qy 139 ACTGAAGGAAGGAGCTCGTCATTCCTCCGCGGTTACGTCACCTAACATCACTGTTACT 198  
Db |||||

Qy 445 ACTGAAGGAAGGAGCTCGTCATTCCTCCGCGGTTACGTCACCTAACATCACTGTTACT 504  
Db |||||

Qy 199 TTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAACCGATATCTGGACAGT 258  
Db |||||

Qy 505 TTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAACCGATATCTGGACAGT 564  
Db |||||

Qy 259 AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db |||||

Qy 565 AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Db |||||

Qy 319 GCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACATCGCAACCAATACA 378  
Db |||||

Qy 625 GCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACATCGCAACCAATACA 684  
Db |||||

Qy 379 ATCATAGATGGTTCGTAGTCCGCTCTCATGGATTGAACTATCTGTTGGAGAAAGCTT 438  
Db |||||

Qy 685 ATCATAGATGGTTCGTAGTCCGCTCTCATGGATTGAACTATCTGTTGGAGAAAGCTT 744  
Db |||||

Qy 439 GTCCTTAAATTTGTACAGCAAGACTGAACATAATGTGGGATTTGACTTCAACTGGGAATAC 498  
Db |||||

Qy 745 GTCTCAATTTGACTGCTACACTCCCTTGAACACGAGAGTTCAANTGACCTGAGGTAC 804  
Db |||||

Qy 499 CTTCTTCGAGAGCATCAGCATAGAAGAACTTGTAAACCGAGACCTTAAACCCGAGTGC 558  
Db |||||

Qy 805 CTTGATGAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTTGACCAAGCAATTC--- 860  
Db |||||

Qy 559 AGTGAGATGAAGAAATTTTGAGCACCTTAAGTATAGTGTGTAAACCGAGTGCACAA 618  
Db |||||

Qy 861 ---CCATGCCACATATTTACAGTGTCTTACTATTGACAAATTCGAGAACAAAGACAAA 918  
Db |||||

Qy 619 GGATTTGACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGACAGCACATTTGTC 678  
Db |||||

Qy 919 GGACTTTATATCTTGTGTTAAGGAGTGGACCATCATTCATCTGTTAACACCTCAGTG 978  
Db |||||

Qy 679 AGGTGTCATGAAA-----GGACAAACTTCACACATGC 711  
Db |||||

Qy 979 CATATATATATAAGACAGGCGCGGGCGAGCCCAAAATCTTGTGACAAAACTTCACACATGC 1038  
Db |||||

Qy 712 CCACGTCGCCAGCAGCTGAACTCTGGGGGACGTCAGTCTTCTCTCCGCCCAAAA 771  
Db |||||

Qy 1039 CCACGTCGCCAGCAGCTGAACTCTGGGGGACGTCAGTCTTCTCTCCGCCCAAAA 1098  
Db |||||

Qy 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTG 831  
Db |||||

Qy 1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTG 1158  
Db |||||

Qy 832 AGCCACGAAGACCTTGAGGTCAAGTTCAATGTTGATCGTGGACGCGGTGGAGGTGCAAT 891  
Db |||||

Qy 1159 AGCCACGAAGACCTTGAGGTCAAGTTCAATGTTGATCGTGGACGCGGTGGAGGTGCAAT 1218  
Db |||||

Qy 892 GCCAAGCAAGCCGCGGAGGACGATACACAGCAGTACCGTGGTGGTGGAGGTGCTC 951  
Db |||||

Qy 1219 GCCAAGCAAGCCGCGGAGGACGATACACAGCAGTACCGTGGTGGTGGAGGTGCTC 1278  
Db |||||

Qy 952 ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAACAAA 1011  
Db |||||

Db 1279 ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAGTGCRAAGGTCTCCAACAAA 1338  
Qy 1012 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAAGGGGAGGCCCGGAGAACCA 1071  
Db |||||

Db 1339 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAAGGGGAGGCCCGGAGAACCA 1398  
Qy 1072 CAGGTGTACACCCCTGCCCCCATCCCGGATGAGTGAACCAAGAACCAAGGTCAAGCTGACC 1131  
Db 1399 CAGGTGTACACCCCTGCCCCCATCCCGGATGAGTGAACCAAGAACCAAGGTCAAGCTGACC 1458  
Qy 1132 TGCCTGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCAG 1191  
Db 1459 TGCCTGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCAG 1518  
Qy 1192 CCGGAGAAACAACTAAGAACACCGCTCCCGTGGTGAATCCCGACGGCTCTTCTTCTCCTC 1251  
Db 1519 CCGGAGAAACAACTAAGAACACCGCTCCCGTGGTGAATCCCGACGGCTCTTCTTCTCCTC 1578  
Qy 1252 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAACGTTCTCATGCTCC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAACGTTCTCATGCTCC 1638  
Qy 1312 GTGATGATGAGGCTCTGCAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCCGGT 1371  
Db 1639 GTGATGATGAGGCTCTGCAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCCGGT 1698  
Qy 1372 AAATGA 1377  
Db 1699 AAATGA 1704

RESULT 15  
AAA91077  
ID AAA91077 standard; DNA; 1704 BP.  
XX  
XX AAA91077;  
XX AC  
XX AC  
DT 05-APR-2001 (first entry)  
XX  
DE Flt1 receptor protein Flt1(1-3)-Fc coding sequence.  
XX  
XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
XX Unidentified.  
OS  
XX  
FH Key Location/Qualifiers  
CDS 1..1704  
FT /\*tag= a  
FT /product= "Flt1(1-3)-Fc"  
XX  
FN W020075319-A1.  
XX  
XX 14-DEC-2000.  
XX  
XX 23-MAY-2000; 2000WO-US014142.  
XX  
XX 08-JUN-1999; 99US-0138133P.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX WPI; 2001-071076/08.  
DR P-PSDB; AAY97597.  
XX  
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX Example 11; Fig 10; 159pp; English.  
XX

CC This sequence encodes a fusion protein of the invention between the Flt1  
CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
CC permeability in a mammal

XX SQ Sequence 1704 BP; 508 A; 460 C; 386 G; 350 T; 0 U; 0 Other;

Query Match 71.2%; Score 980.8; DB 5; Length 1704;  
Best Local Similarity 85.3%; Pred. No. 7.8e-228;  
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;

QY	79	AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTAACACATG	138
DB	385	AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTAACACATG	444
QY	139	ACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGTTACCGTCACTTAACATCACTGTACT	198
DB	445	ACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGTTACCGTCACTTAACATCACTGTACT	504
QY	199	TTAAAAAAGCTTCCACTTCACACTTTGATCCCTGATGGAACGCATATCTGGACAGT	258
DB	505	TTAAAAAAGCTTCCACTTCACACTTTGATCCCTGATGGAACGCATATCTGGACAGT	564
QY	259	AGAAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATAGGGCTTCTGACCTGTGAA	318
DB	565	AGAAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATAGGGCTTCTGACCTGTGAA	624
QY	319	GCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACATCGACAAACCAATACA	378
DB	625	GCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACATCGACAAACCAATACA	684
QY	379	ATCATAGATGGTCTGAGTCCGTCTCATGGAATGAACATATCTGTGGAGAAAGCTT	438
DB	685	ATCATAGATGGTCCAAATAAGCACACACCGCCAGTCAAAATTTAGAGGCCATCTCTT	744
QY	439	GTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATTTGACTTCAACTGGGAATAC	498
DB	745	GTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATTTGACTTCAACTGGGAATAC	804
QY	499	CTTCTTTCGAAGCATCAGCATAGAAACTTTGTAACCGGAGACCTTAAACCCAGTCTGGG	558
DB	805	CTTCTTTCGAAGCATCAGCATAGAAACTTTGTAACCGGAGACCTTAAACCCAGTCTGGG	858
QY	559	AGTGAGATGAAGAAATTTTGTAGACCTTAACTATAGATGGTGTAAACCGGAGTGACCAA	618
DB	859	AGTGAGATGAAGAAATTTTGTAGACCTTAACTATAGATGGTGTAAACCGGAGTGACCAA	918
QY	619	GGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGACGACATTTGTC	678
DB	919	GGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGACGACATTTGTC	978
QY	679	AGGGTCCATGAAAA-----GGACAAAACTCACACATGC	711
DB	979	CATATATATGATAAAGCAGCGCGCGAGCCCAAAATCTTGTGACAAAACTCACACATGC	1038
QY	712	CCACGTCGCCAGCACTGAACTCTCTGGGGGAGCGTCACTCTTCTCTTCCCGCCAAAA	771
DB	1039	CCACGTCGCCAGCACTGAACTCTCTGGGGGAGCGTCACTCTTCTCTTCCCGCCAAAA	1098
QY	772	CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCCACATCGTGGTGGTGGACGTG	831
DB	1099	CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCCACATCGTGGTGGTGGACGTG	1158
QY	832	AGCCACGAGACCTCTGAGTCAAGTTCAACTGGTACGTGGACGGCGGTGGAGGTGCATAAT	891
DB	1159	AGCCACGAGACCTCTGAGTCAAGTTCAACTGGTACGTGGACGGCGGTGGAGGTGCATAAT	1218
QY	892	GCCAAAGAAAGCGCGGAGGAGGAGTACAAACAGCATACCGTGTGGTCAAGCGTCTCTC	951
DB	1219	GCCAAAGAAAGCGCGGAGGAGGAGTACAAACAGCATACCGTGTGGTCAAGCGTCTCTC	1278

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Job time : 795.087 secs

QY	952	ACCGTCTCGCACAGGACTGGCTGAATGCGCAAGGAGTACAAAGTCAAGGTCTTCCAAACAA	1011
DB	1279	ACCGTCTCGCACAGGACTGGCTGAATGCGCAAGGAGTACAAAGTCAAGGTCTTCCAAACAA	1338
QY	1012	GCCCTCCAGGCCCCCATCGAGAAAAACCATCTCTCCAAAGCCAAAGGGCAGCCCGAGAACCA	1071
DB	1339	GCCCTCCAGGCCCCCATCGAGAAAAACCATCTCTCCAAAGCCAAAGGGCAGCCCGAGAACCA	1398
QY	1072	CAGGTGTACACCTGSCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCC	1131
DB	1399	CAGGTGTACACCTGSCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCC	1458
QY	1132	TGCCTGGTCAAAAGGCTTCTATCCCAAGCAGCATCGCGTGGAGTGGAGAGCAATGGGCAG	1191
DB	1459	TGCCTGGTCAAAAGGCTTCTATCCCAAGCAGCATCGCGTGGAGTGGAGAGCAATGGGCAG	1518
QY	1192	CCGAGAAACAACTACAAGACACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTC	1251
DB	1519	CCGAGAAACAACTACAAGACACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTC	1578
QY	1252	TACAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGGGGAAAGCTTCTCTCATGCTCC	1311
DB	1579	TACAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGGGGAAAGCTTCTCTCATGCTCC	1638
QY	1312	GTGATGATGAGGCTTCTGCACAAACCACTACACGCAAGAGAGCTCTCCTGTCTCGGGT	1371
DB	1639	GTGATGATGAGGCTTCTGCACAAACCACTACACGCAAGAGAGCTCTCCTGTCTCGGGT	1698
QY	1372	AAATGA 1377	
DB	1699	AAATGA 1704	

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 21:19:06 ; Search time 4869.12 Seconds  
(without alignments)  
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Title: US-10-009-852-15  
Perfect score: 1377  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc3:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	49.7	871	4	BG753979 602709506
2	684	49.7	983	5	BQ708975 AGENCOURT
3	683	49.6	941	5	BQ712021 AGENCOURT
4	682.4	49.6	843	4	BM007897 603617582
5	682.4	49.6	925	5	BQ709152 AGENCOURT
6	682.4	49.6	1022	3	CR611254 full-leng
7	682.4	49.6	1048	3	CR595172 full-leng
8	682.4	49.6	1090	3	CR612308 full-leng
9	682.4	49.6	1091	3	CR604961 full-leng
10	682.4	49.6	1093	3	CR616804 full-leng
11	682.4	49.6	1098	3	CR626477 full-leng
12	682.4	49.6	1100	3	CR612813 full-leng
13	682.4	49.6	1102	3	CR601777 full-leng
14	682.4	49.6	1102	3	CR625051 full-leng
15	682.4	49.6	1103	3	CR595194 full-leng
16	682.4	49.6	1104	3	CR591904 full-leng
17	682.4	49.6	1106	3	CR613460 full-leng
18	682.4	49.6	1106	3	CR620071 full-leng
19	682.4	49.6	1107	3	CR598548 full-leng
20	682.4	49.6	1109	3	CR614200 full-leng
21	682.4	49.6	1109	3	CR619687 full-leng
22	682.4	49.6	1111	3	CR606782 full-leng
23	682.4	49.6	1114	3	CR593349 full-leng
24	682.4	49.6	1114	3	CR618075 full-leng

ALIGNMENTS

RESULT 1  
BG753979 602709506F1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4846201 5',  
LOCUS mRNA sequence.  
DEFINITION BG753979.1 GI:14064632  
ACCESSION BG753979  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: LLCM1686 row: k column: 02  
High quality sequence stop: 848.  
Location/Qualifiers  
1. 871  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4846201"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 48"  
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

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CR619868 full-leng  
CR611468 full-leng  
CR598462 full-leng  
CR598316 full-leng  
CR607277 full-leng  
CR611016 full-leng  
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BX346946 BX346946  
BQ706204 AGENCOURT  
BQ709339 AGENCOURT  
BQ709771 AGENCOURT  
BX360518 BX360518  
BQ709144 AGENCOURT  
BG674795 602620925  
BQ712363 AGENCOURT  
BQ711291 AGENCOURT  
BG397723 602438784  
BM008412 603617406  
BX367600 BX367600  
BQ709859 AGENCOURT



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QY 1354 CTCTCCCTGTCTCCGGTAAATGA 1377
Db 684 CTCTCCCTGTCTCCGGTAAATGA 707

RESULT 3
LOCUS BQ712021
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
5', mRNA sequence.
ACCESSION BQ712021
VERSION BQ712021
KEYWORDS BQ712021.1 GI:21850920
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.
Location/Qualifiers
1. 941
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/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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## ORIGIN

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Query Match 49.6%; Score 683; DB 5; Length 941;
Best Local Similarity 99.9%; Pred. No. 9.2e-179;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTGCCAGCACCTGAACTCTGGGGGACCGTCAGTC 753
Db 50 GACAAACTCACATGCCACCGTGCCAGCACCTGAACTCTGGGGGACCGTCAGTC 109

QY 754 TTCTCTTCCCGCCAAACCCAGAGACCCCTCATGATCTCCGAGACCCCTGAGGTACA 813
Db 110 TTCTCTTCCCGCCAAACCCAGAGACCCCTCATGATCTCCGAGACCCCTGAGGTACA 169

QY 814 TGCGTGTGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db 170 TGCGTGTGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

QY 874 GGCGTGGAGGTGCATAATGCCAAGCAAGCGCGGAGGAGCAGTACAACAGCAGCTAC 933
Db 230 GGCGTGGAGGTGCATAATGCCAAGCAAGCGCGGAGGAGCAGTACAACAGCAGCTAC 289

QY 934 CGTGTGTGTCAGGCTCCTCACCCTCTGACCAAGGACTGGCTGAATGGCAAGGATACAAG 993
Db 290 CGTGTGTGTCAGGCTCCTCACCCTCTGACCAAGGACTGGCTGAATGGCAAGGATACAAG 349
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QY 994 TGCAGGCTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACACCTCTCCAAAGCCAAA 1053
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QY 1054 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113
Db 410 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 469

QY 1114 AACCAAGTCAAGCTGAGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATGCCGTGGAG 1173
Db 470 AACCAAGTCAAGCTGAGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATGCCGTGGAG 529

QY 1174 TGGGAGAGCAATGGCGAGCCGAGAACAACTACAGACACCGCTCCCGTGTGACTCC 1233
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QY 1234 GACGGCTCTTTCTTCTCTACAGCAAGCTACCGTGGGCAAGAGCAGGTGGCAGCGGG 1293
Db 590 GACGGCTCTTTCTTCTCTACAGCAAGCTACCGTGGGCAAGAGCAGGTGGCAGCGGG 649

QY 1294 AACGCTCTCTCATGCTCCGTCATGCATGAGGCTCTGCACACCACTACACGAGAGAGC 1353
Db 650 AACGCTCTCTCATGCTCCGTCATGCATGAGGCTCTGCACACCACTACACGAGAGAGC 709

QY 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
Db 710 CTCTCCCTGTCTCCGGGTAAATGA 733

RESULT 4
LOCUS BM007897
DEFINITION 603617582P1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
mRNA sequence.
ACCESSION BM007897
VERSION BM007897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.
Location/Qualifiers
1. 843
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

Query Match 49.6%; Score 682.4; DB 4; Length 843;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCCGGGGACCGTCAAGTC 753  
Db 108 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCCGGGGACCGTCAAGTC 167

Qy 754 TTCTCTTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAACA 813  
Db 168 TTCTCTTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAACA 227

Qy 814 TGCCTGTGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGTTAGTCACTGGAC 873  
Db 228 TGCCTGTGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGTTAGTCACTGGAC 287

Qy 874 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAGGAGTACACAGCACCTGAC 933  
Db 288 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAGGAGTACACAGCACCTGAC 347

Qy 934 CGTGTGTGTGAGCTCTCACCGTCTGTCACAGGAGTGGTGAATGGCAAGGAGTACAAG 993  
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Qy 994 TGCAGGTCTTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
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Qy 1174 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACAGCTCTCCGCTGGAGTCC 1233  
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Qy 1294 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1353  
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RESULT 5  
BQ709152  
LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCO152 NIH\_MGC\_113 Homo sapiens cdna clone IMAGE:6301245  
5', mRNA sequence.  
ACCESSION BQ709152  
VERSION BQ709152.1 GI:21848051  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 925)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Cloned Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LCM2516 row: m column: 22  
High quality sequence stop: 739.

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/organism="Homo sapiens"  
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/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 49.6%; Score 682.4; DB 5; Length 925;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCCGGGGACCGTCAAGTC 753  
Db 48 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCCGGGGACCGTCAAGTC 107

Qy 754 TTCTCTTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAACA 813  
Db 108 TTCTCTTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAACA 167

Qy 814 TGCCTGTGTGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGTTAGTCACTGGAC 873  
Db 168 TGCCTGTGTGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGTTAGTCACTGGAC 227

Qy 874 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAGGAGTACACAGCACCTGAC 933  
Db 228 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAGGAGTACACAGCACCTGAC 287

Qy 934 CGTGTGTGTGAGCTCTCACCGTCTGTCACAGGAGTGGCTGAATGGCAAGGAGTACAAG 993  
Db 288 CGTGTGTGTGAGCTCTCACCGTCTGTCACAGGAGTGGCTGAATGGCAAGGAGTACAAG 347

Qy 994 TGCAGGTCTTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCACTCTCCAAAGCCAAA 1053  
Db 348 TGCAGGTCTTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCACTCTCCAAAGCCAAA 407

Qy 1054 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCCTCCATCCCGGGAGTGGTCAACCAAG 1113  
Db 408 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCCTCCATCCCGGGAGTGGTCAACCAAG 467

Qy 1114 AACCAGGTTCAGCTGACCTGCTGCTCAAGGCTTTCTATCCAGCGACATCGCCGTGGAG 1173  
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Qy 1174 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACAGCTCTCCGCTGGAGTCC 1233  
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Qy 1234 GACGCTCTTCTTCTCTACAGAGCTACCGTGGCAAGAGCAGTGGCGACAGGG 1293  
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Qy 1294 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1353  
Db 708 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1353



Db 648 AACGCTTCTCAGTCCCGTGAATGATGAGGCTCTGCACAACCACTACACAGAGAAGC 707

Qy 1354 CTCTCCCTGCTCCGGTAAATGA 1377

Db 708 CTCTCCCTGCTCCGGTAAATGA 731

RESULT 6

LOCUS CR611254 1022 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens (human).

ACCESSION CR611254

VERSION CR611254.1 GI:50492061

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2 (bases 1 to 1022)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

1..1022

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DE007YJ17"

/tissue\_type="Placenta"

/plasmid="pCMVSPORT\_6"

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 1.4e-178;

Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAAACCTCACATGCCACCGTGCACGACCTGAACTCCTGGGGGACCGTCAGTC 753

Db 323 GACAAAACCTCACATGCCACCGTGCACGACCTGAACTCCTGGGGGACCGTCAGTC 382

Qy 754 TTCTCTTCCCCCAAAACCAAGACACCTCATGATCTCCGACCCCTGAGGTACA 813

Db 393 TTCTCTTCCCCCAAAACCAAGACACCTCATGATCTCCGACCCCTGAGGTACA 442

Qy 814 TGGTGGTGGTGGAGCGTGAAGCAGCAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAC 873

Db 443 TGGTGGTGGTGGAGCGTGAAGCAGCAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy 874 GGGTGGAGGTGCATAAATGCCNAGCAAAAGCGGGGAGGAGCAGTACACAGACACGTAC 933

Db 503 GGGTGGAGGTGCATAAATGCCNAGCAAAAGCGGGGAGGAGCAGTACACAGACACGTAC 562

Qy 934 CGTGGTGCAGGTCTCTCACCGTCTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAG 993

Db 563 CGTGGTGCAGGTCTCTCACCGTCTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAG 622

Qy 994 TGCAGGTCTCCAAACAAAGCCCTCCACGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 1053

Db 623 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 682

Qy 1054 GGGCAGCCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113

Db 683 GGGCAGCCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 742

Qy 1114 AACCAGGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCGTGGAG 1173

Db 743 AACCAGGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCGTGGAG 802

Qy 1174 TGGGAGAGCAATGGGAGCGGAGAGAACATACAGACCAAGCTCCCGTCTGCTGACTCC 1233

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Db 863 GACGCTCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGAGCAGGTGCAGCAGGG 922

Qy 1294 AACGCTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACACAGAGAAGC 1353

Db 923 AACGCTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACACAGAGAAGC 982

Qy 1354 CTCTCCCTGCTCCGGGTAATGA 1377

Db 983 CTCTCCCTGCTCCGGGTAATGA 1006

RESULT 7

LOCUS CR595172 1048 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION CR595172

VERSION CR595172.1 GI:50475979

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2 (bases 1 to 1048)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

1..1048

/organism="Homo sapiens"

/mol\_type="mRNA"

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/tissue\_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT\_6"

ORIGIN

Query Match 49.6%; Score 682.4; DB 3; Length 1048;

Best Local Similarity 99.9%; Pred. No. 1.4e-178;

Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAAACCTCACATGCCACCGTGCACGACCTGAACTCCTGGGGGACCGTCAGTC 753



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VERSION      CR604961.1  GI:50485768
KEYWORDS     HTC; CNSLT cDNA.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1091)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK       Contact: Feng Liang Email: fliang@lifetech.com URL:
             http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
             Faraday Avenue
             Genoscope.
REFERENCE    2 (bases 1 to 1091)
AUTHORS      Direct Submission
TITLE        Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
             - Web: www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
             was normalized. Library was constructed by Life Technologies, a
             division of Invitrogen.
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ACCESSION CR616804
VERSION    CR616804.1 GI:50497611
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SOURCE     Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1093)
AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished
REMARK     Contact: Feng Liang Email: fliang@lifetech.com URL:
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
            Genoscope.
REFERENCE  2 (bases 1 to 1093)
AUTHORS    Direct Submission
TITLE      Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL    BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
            - Web: www.genoscope.cns.fr)
COMMENT    1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAAACCTCACATGCCACCGTGCACGACCTGAACTCTCTGGGGGGACCGTCAGTC 753
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REFERENCE 2 (bases 1 to 1100)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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VERSION HTc; CNSLT cDNA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1102)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
Genoscope.
2 (bases 1 to 1102)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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division of Invitrogen.
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Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 5.1.6  
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ALIGNMENTS

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; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 25  
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Qy	1012	GCCTCTCCAGCCGCCCATCGAGAAAACCATCTCCAAAGCCAAAGCGCAGCCCGAGAACCA	1071
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Qy	1072	CAGGTGTACACCTGTGCCCCCATCCCGGGATGAGCTGACCAAAGAACGAGTCAGCTTGACC	1131
Db	1140	CAGGTGTACACCTGTGCCCCCATCCCGGGATGAGCTGACCAAAGAACGAGTCAGCTTGACC	1199
Qy	1132	TGCCTGTGTCAAAGGCTTCTATCCCGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG	1191
Db	1200	TGCCTGTGTCAAAGGCTTCTATCCCGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG	1259
Qy	1192	CCGGAGAACAACTACAAGACACCGCTCCCGTGTGTGACTCCGACGGCTCTTCTTCTCCTC	1251
Db	1260	CCGGAGAACAACTACAAGACACCGCTCCCGTGTGTGACTCCGACGGCTCTTCTTCTCCTC	1319
Qy	1252	TACAGCAGCTCACCGTGGACAAGACAGGTGGCAGCAGGGGAAAGCTTCTTCATGCTCC	1311
Db	1320	TATAGCAAGCTCACCGTGGACAAGACAGGTGGCAGCAGGGGAAAGCTTCTTCATGCTCC	1379
Qy	1312	GTGATGATCAGGCTGTGCACAACCACTACACCGAAGAGCCTCTCCCTGTCTCCGGGT	1371
Db	1380	GTGATGATCAGGCTGTGCACAACCACTACACCGAAGAGGCTCTCCCTGTCTCCGGGT	1439
Qy	1372	AAATGA	1377
Db	1440	AAATGA	1445

### RESULT 3

US-09-773-877B-23

US-09-773-877B-23  
: Sequence 23, Application US/09773877B

; Patent No. 6833349

; FISCAL NO. 003343  
; GENERAL INFORMATION:

; APPLICANT: Xia, Yu-Ping et al.

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

; FILE REFERENCE: REG 710b

; CURRENT APPLICATION NUMBER: US/09/773,877B

; CURRENT FILING DATE: 2001-01-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version

; SEQ ID NO 23

; LENGTH: 1444

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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; ORGANISM: Artificial Sequence  
FEATURE:

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FEATURE:
;
OTHER INFORMATION: F1+1D2 VECEPD3 EcdeltaC1 (a) percent

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; OTHER INFORMATION: Flt1D2, VEGFR3D3, FcdeltaC1(a)Receptor
: NAME/KEY: CDS
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; NAME/KEY: CDS
; LOCATION: (69) (1436)

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LOCATION: (69) .. (1436)  
IIS-09-773-877B-23

67-811-60-20

Query Match	Score	DB 4:	Length
76.2%	1049.2	DB 4:	Length 1444:

Query Match 70.2%; Score 1043.2; DS 4; Length 1444;  
Best Local Similarity 86.7%; Pred. No. 6.7e-271;

Matches 1201; Conservative 0; Mismatches 158; Indels 27; Gaps 3;

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Qy 1 ATGTCAGCTACTGGGACACCGGGTCTGTCTGTGCGGCTGCTCAGCTGTCTGCTTCTC 60

[illegible]

Db 1131 CAGGTGTACACCTGCGCCCTCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGACC 1190  
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Db 1191 TGCCTGGTCAAGGGCTTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGGCAG 1250  
Qy 1192 CCGGAGAACAACTACAAGACCAACGCTCCCGTGGTGGACTCGGAGGGCTCTTCTCTC 1251  
Db 1251 CCGGAGAACAACTACAAGACCAACGCTCCCGTGGTGGACTCGGAGGGCTCTTCTCTC 1310  
Qy 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGAGGGGAAAGCTTCTCATGTCTC 1311  
Db 1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGAGGGGAAAGCTTCTCATGTCTC 1370  
Qy 1312 GTGATGATAGGCTCTGCAAAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCGGGT 1371  
Db 1371 GTGATGATAGGCTCTGCAAAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCGGGT 1430  
Qy 1372 AAATGA 1377  
Db 1431 AAATGA 1436

RESULT 4

US-09-773-877B-15  
; Sequence 15, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 1359  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc1(2-3 deltaB) -Fc (Mut2)  
; NAME/KEY: CDS  
; LOCATION: (1)...(1359)  
US-09-773-877B-15

Query Match 75.5%; Score 1039; DB 4; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 3.5e-268;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

Qy 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGGTGCTCAGTGTCTGCTCTC 60  
Db 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGGTGCTCAGTGTCTGCTCTC 60  
Qy 61 ACAGATCTAGTCTCGGAAGTGATACCGGTAGACCTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGATCTAGTCTCGGA-----GGTAGACTTTCGTAGAGATGTACAGTGAATC 111  
Qy 121 CCCGAAATTATACATGACTGAAGGAGGAGTGTGCTCATTCCTGCCGGTTTACGTCA 180  
Db 112 CCCGAAATTATACATGACTGAAGGAGGAGTGTGCTCATTCCTGCCGGTTTACGTCA 171  
Qy 181 CCTAACATCACTGTACTTTAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAA 240  
Db 172 CCTAACATCACTGTACTTTAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAA 231  
Qy 241 CGCATAACTCGGACAGTAGAAGGGCTTCATCATATCAAACTGCAAGTCAAGAAATA 300  
Db 232 CGCATAACTCGGACAGTAGAAGGGCTTCATCATATCAAACTGCAAGTCAAGAAATA 291  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 360  
Db 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 351

RESULT 5  
US-09-773-877B-17  
; Sequence 17, Application US/09773877B  
; Patent No. 6833349

Qy 361 CATCGACAAACCAATACATAGATGTGGTCTGAGTCCGTCTCATGGAATTTGAAC 420  
Db 352 CATCGACAAACCAATACATAGATGTCAAATAAGCACACACCCCGAGTCAAAATTA 411  
Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATTTGGGGATT 480  
Db 412 CTTAGAGCCATCTCTTGTCTCAATTTGCTGTACCACTCCCTTTGAAACACAGAGTT 471  
Qy 481 GACTTCAACTGGGAATACCCCTTTTCGAAGCATCAGCATAGAAATTTGTAAACCGAGAC 540  
Db 472 CAATGACCTGGAGTTACCTCTGATGAATTTGACAAAGCAATTCCTCATGCCAATATTC 531  
Qy 541 CTAAACCCAGCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGGT 600  
Db 532 TACAGTGTCTTACTATTGTAACAAATGCAAGCAAAAGCAAAAGAGACTTTTACTTTGCT 591  
Qy 601 GTAAACCCGAGTGACCAAGGATTTACACCTGTGTGACGATCCAGTGGGCTGATGCCAAG 660  
Db 592 GTAA--GGAGTGGACCATCAATCAATCTGTTAAACACCTC-----AGTGCAATATAT 642  
Qy 661 AAGAACAGCACATTTGTGAGGGTCCATGAAAGAGCAAAACTCACATGCCACCGTGC 720  
Db 643 GATAAAGCAGGCCCGGGCGAGCCCAATCTTGTGACAAAACTCACACATGCCACCGTGC 702  
Qy 721 CCAGCCTGAACTCTCCCGGACCCCTGAGGTCAATGCTGCTGGTGGAGCTGAGCCAGAA 840  
Db 763 ACCCTCATGATCTCCCGGACCCCTGAGTCAATGCTGCTGGTGGAGCTGAGCCAGAA 822  
Qy 841 GACCTGAGTCAAGTTTCACTGCTGAGCGGCTGAGGAGTGCATTAATGCAAGACA 900  
Db 823 GACCTGAGTCAAGTTTCACTGCTGAGCGGCTGAGGAGTGCATTAATGCAAGACA 882  
Qy 901 AAGCGCGGAGGAGGAGTACACGACGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 883 AAGCGCGGAGGAGGAGTACACGACGTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942  
Qy 961 CACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGGCTTCCCAACAAAGCCCTCCCA 1020  
Db 943 CACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGGCTTCCCAACAAAGCCCTCCCA 1002  
Qy 1021 GCCCCATCGAGAAACCACTCTCAAAGCAAAGGGCAGCCCCGAGAACCAACAGGTGAC 1080  
Db 1003 GCCCCATCGAGAAACCACTCTCAAAGCAAAGGGCAGCCCCGAGAACCAACAGGTGAC 1062  
Qy 1081 ACCCTGCCCATCCCGGGATGAGTGAACCAAGAACAGGCTGAGCTGACCTGCTGCTGCTC 1140  
Db 1063 ACCCTGCCCATCCCGGGATGAGTGAACCAAGAACAGGCTGAGCTGAGCTGCTGCTGCTC 1122  
Qy 1141 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGGGAAC 1200  
Db 1123 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGGGAAC 1182  
Qy 1201 AACTAAGACACAGCTCCCGTGTGGAATCCGAGCGGCTCTTCTTCTCTTACAGCAAG 1260  
Db 1183 AACTAAGACACAGCTCCCGTGTGGAATCCGAGCGGCTCTTCTTCTCTTACAGCAAG 1242  
Qy 1261 CTCAACGTCGACAGAGCAGGTGGCAGCGGGAAAGCTTCTCATGCTCCGCTGATGCAT 1320  
Db 1243 CTCAACGTCGACAGAGCAGGTGGCAGCGGGAAAGCTTCTCATGCTCCGCTGATGCAT 1302  
Qy 1321 GAGGCTCTGCACACCACTACAGCGAAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 1303 GAGGCTCTGCACACCACTACAGCGAAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1359

QY 79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138

||||| 385 AGTGATACAGGTAGACCTTTTCGTAGAGATGATACAGTGAATATCCCGAAATATACATG 444  
Qy 139 ACTGAAGGAAGGAGCTCGTCAITCCCTGCGGGTTAGCTCACCTAAACATCACTGTTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCAITCCCTGCGGGTTAGCTCACCTAAACATCACTGTTACT 504  
Qy 199 TTAAGAAAGTTTCACCTTGACACTTTGATCCCTGATGGAAGAAACGCATTAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCACCTTGACACTTTGATCCCTGATGGAAGAAACGCATTAATCTGGGACAGT 564  
Qy 259 AGAAGGCTTCATCATATCAATCAAAATGCAAGCTGACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGCTTCATCATATCAATCAAAATGCAAGCTGACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGATAAGACAAATCTCTCACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGATAAGACAAATCTCTCACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGGTTCTGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGAGAAAGCTT 438  
Db 685 ATCATAGATGGTTCTGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGAGAAAGCTT 744  
Qy 439 GTCTTAAATCTACAGCAAGAACTGAATTAATGTTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCTAATTTGACTGCTACCACTCCCTTGAACAGAGAGTTCAATGACCTGGAGTTAC 804  
Qy 499 CCTTCTTGAAAGCATCAGCATAAGAACTTTGAAACCGAGACCTTAAACCCAGCTCTGGG 558  
Db 805 CCTGATGAATTTGACCAAGCAATTCCTCATGCCAATATTTCTACAGTTTCTTACTATT 864  
Qy 559 AGTGAGATGAAGAAATTTTGGAGCACTTAACTATAGATGGTGTAAACCGGAGTGACAA 618  
Db 865 GACAAATGCAAGAAACAAAGACAAGAGACTTTATCTTGTCTGTGAA---GGAGTGGACCA 921  
Qy 619 GGATTTGATACCTGTGAGCATCCAGTGGGCTGATGACCAAGAGAAACAGACACATTTGTC 678  
Db 922 TCATTTCAATCTGTTAACCTC-----AGTGATATATATGATAAGAGGCCCGGCG 975  
Qy 679 AGGTTCCATGAAAGGACAAACTCACATGCCCCCGTCCGAGCAACCTGAACTCCTG 738  
Db 976 GAGCCCAATCTTGTGACAAACTCACATGCCCCCGTCCGAGCAACCTGAACTCCTG 1035  
Qy 739 GGGGAGCGTCACTTCTCTTCCCGCAAAACCCAGGACACCTCATGATCTCCGG 798  
Db 1036 GGGGAGCGTCACTTCTCTTCCCGCAAAACCCAGGACACCTCATGATCTCCGG 1095  
Qy 799 ACCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCAAGACCTTGAGTCAAGTTC 858  
Db 1096 ACCCTGAGGTACATGCGTGGTGGAGCTGAGCCAGCAAGACCTTGAGTCAAGTTC 1155  
Qy 859 AACTGGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAG 918  
Db 1156 AACTGGTACGTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAG 1215  
Qy 919 TACAACAGCATACCGTGGTGGAGTCCCTACCGTCTGACAGGACTGCTGAAT 978  
Db 1216 TACAACAGCATACCGTGGTGGAGTCCCTACCGTCTGACAGGACTGCTGAAT 1275  
Qy 979 GGCAGAGGTACAAGTGAAGGTCTTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAACC 1038  
Db 1276 GGCAGAGGTACAAGTGAAGGTCTTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAACC 1335  
Qy 1039 ATCTCCAAAGCCAAAGGCGAGCCCGAGAAACACAGGTGTACACCTGCCCGCCATCCCGG 1098  
Db 1336 ATCTCCAAAGCCAAAGGCGAGCCCGAGAAACACAGGTGTACACCTGCCCGCCATCCCGG 1395  
Qy 1099 GATGAGTGAACCAAGAACCGAGTCAAGCTGACCTGCTGCTGCTCAAGGGCTTCTATCCAGC 1158  
Db 1396 GATGAGTGAACCAAGAACCGAGTCAAGCTGACCTGCTGCTGCTCAAGGGCTTCTATCCAGC 1455  
Qy 1159 GACATCGCGTGGAGTGAGCAATGGGCGAGCGGAGGAACTTCAAGACCCAGCCT 1218  
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Db 1456 GACATCCCGTGGAGTGGGAGAGCAATGGCAGCGGAGAAACAACTACAGACCAACGCT 1515  
Qy 1219 CCGTGTCTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGC 1278  
Db 1516 CCGTGTCTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGC 1575  
Qy 1279 AGTGGCAGCAGGGAAGCTTCTCTCATGCTCCGTTGATGATGAGGCTCTGCAACCAAC 1338  
Db 1576 AGTGGCAGCAGGGAAGCTTCTCTCATGCTCCGTTGATGATGAGGCTCTGCAACCAAC 1635  
Qy 1339 TACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1377  
Db 1636 TACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1674  
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RESULT 7

US-09-773-877B-19  
; Sequence 19, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 1704  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1 (1-3 R->N) (Mut 4)  
; NAME/KEY: CDS  
; LOCATION: (1)..(1704)  
US-09-773-877B-19

Query Match 71.3%; Score 982.4; DB 4; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 5,7e-253;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;  
Qy 79 AGTGATACCGGTAGACCTTTTCGTAGAGATGATGAGTGAATATCCCGAAATATACATG 138  
Db 385 AGTGATACAGGTAGACCTTTTCGTAGAGATGATGAGTGAATATCCCGAAATATACATG 444  
Qy 139 ACTGAAGGAAGGAGCTCGTCAITCCCTGCGGGTTACGTCACCTAAACATCACTGTTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCAITCCCTGCGGGTTACGTCACCTAAACATCACTGTTACT 504  
Qy 199 TTAAGAAAGTTTCACCTTGACACTTTGATCCCTGATGGAAGAAACGCATTAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCACCTTGACACTTTGATCCCTGATGGAAGAAACGCATTAATCTGGGACAGT 564  
Qy 259 AGAAGGCTTCATCATATCAATCAAAATGCAAGCTGACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGCTTCATCATATCAATCAAAATGCAAGCTGACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGATAAGACAAATCTCTCACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGATAAGACAAATCTCTCACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGGTTCTGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGAGAAAGCTT 438  
Db 685 ATCATAGATGGTTCTGAGTCCGTCTCATGGAATTTGAATCTATCTGAGAGCCATCTCTT 744  
Qy 439 GTCTTAAATTTGACAGCAAGAACTGAATTAATGTTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCTAATTTGACTGCTACCACTCCCTTGAACAGAGAGTTCAATGACCTGGAGTTAC 804  
Qy 499 CCTTCTTGAAAGCATCAGCATAAGAACTTTGTAACCGAGACCTTAAACCCAGCTCTGGG 558  
Db 805 CCTGATGAAAGAAATTAAGAACGCTTCCGTAAGGCGAGCAATTTGACCAAGCAATTC--- 860  
|||||

Qy	559	AGT	GAGATGAAGAAATTTT	TGAGCACCTTA	ACTATAGATCGTGTAAACCCGGAGTGACCAA	618
Db	861	--	CCATGCCAACATATTTCT	CACAGTGTCTT	TACTATATGACAAAATGCGAGAAACAAGACAAA	918
Qy	619	GGATT	GTACACCTGTG	CAGCATCCAGTGGGCTG	ATGACCAAGAAGACACACATTTGTC	678
Db	919	GGACTT	TATACTTGTCTGT	GTAAAGAGTGG	ACCATCATTTCAAATCTGTTAACACTCAGTG	978
Qy	679	AGG	GTCCATGAAAA-----	-----	GGACAAAACTCACATGTC	711
Db	979	CATATATATGATAAAGCAGGCCCCGGGCGAGCCCCAAATCTTGTGACAAAACTCACATGTC	1038			
Qy	712	CCACG	TGCCACGACCTG	AACTCCTCGGGGGACCGTCAGTCTTCTCTTCCCCCAAAA	771	
Db	1039	CCACG	TGCCACGACCTG	AACTCCTCGGGGGACCGTCAGTCTTCTCTTCCCCCAAAA	1098	
Qy	772	CCC	AAAGACACCTCATGATCTCCCGA	CCCCCTGAGGTCA	CATCGTGGTGGTGGACGTG	831
Db	1099	CCC	AAAGACACCTCATGATCTCCCGAC	CCCCCTGAGGTCA	CATCGTGGTGGTGGACGTG	1158
Qy	832	AGCC	ACGAGACCTGAGGTCAAGTTCAA	CTGGTACGTGACCGCGTGGAGGTGCATAT	891	
Db	1159	AGCC	ACGAGACCTGAGGTCAAGTTCAA	CTGGTACGTGACCGCGTGGAGGTGCATAT	1218	
Qy	892	GCCA	AGACAAAGCCGCGGAGGACGAC	TACAAACAGCACGTACCGTGTGGT	CAGCGTCTC	951
Db	1219	GCCA	AGACAAAGCCGCGGAGGACGAC	TACAAACAGCACGTACCGTGTGGT	CAGCGTCTC	1278
Qy	952	ACG	CTCTGCACAGGACTGGCTGAATGGCAAGGAGTAC	AAAGTGCAAGTGTCTCCAA	CAAA	1011
Db	1279	ACG	CTCTGCACAGGACTGGCTGAATGGCAAGGAGTAC	AAAGTGCAAGTGTCTCCAA	CAAA	1338
Qy	1012	GCCT	CCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACCA	1071		
Db	1339	GCCT	CCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACCA	1398		
Qy	1072	CAG	GTGTACACCTCGCCCATCCCGGGATGAGCTGA	CCAAAGAACACAGGT	CAGCCTGACC	1131
Db	1399	CAG	GTGTACACCTCGCCCATCCCGGGATGAGCTGA	CCAAAGAACACAGGT	CAGCCTGACC	1458
Qy	1132	TGC	TGTGTCAAGGCTTCTATCCACGGACATCGCCGTGGAGTGGGAGACCAATGGGCAG	1191		
Db	1459	TGC	TGTGTCAAGGCTTCTATCCACGGACATCGCCGTGGAGTGGGAGACCAATGGGCAG	1518		
Qy	1192	CCG	GAGAACAACTACAAAGACACAGCCTCCCGTGTG	GACTCCGACCTCCGACGGCTCTTCTTCTCTC	1251	
Db	1519	CCG	GAGAACAACTACAAAGACACAGCCTCCCGTGTG	GACTCCGACCTCCGACGGCTCTTCTTCTCTC	1578	
Qy	1252	TAC	AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA	CGTCTTCTCATGCTCC	1311	
Db	1579	TAC	AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAA	CGTCTTCTCATGCTCC	1638	
Qy	1312	GT	ATGATGAGGCTCTG	CACAAACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGT	1371	
Db	1639	GT	ATGATGAGGCTCTG	CACAAACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGT	1698	
Qy	1372	AAATGA	1377			
Db	1699	AAATGA	1704			

SEQ ID NO.	SEQUENCE	SEQUENCE LENGTH	SEQUENCE TYPE	SEQUENCE DESCRIPTION
1035	CCACCGTCTCCAGACACCTCTGAGATCTCCCGGAGCCCTCGAGGTCAATCGTGGTGGACGCTG	831	QY	US-09-773-877B-11
772	CCCAAGGACACCTCATGATCTCCCGGACCCCTCGAGGTCAATCGTGGTGGACGCTG	831	QY	Sequence 11, Application US/09773877B
1099	CCCAAGGACACCTCATGATCTCCCGGACCCCTCGAGGTCAATCGTGGTGGACGCTG	1158	Db	Patent No. 6833349
832	AGCCACGAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGACCGCGCTGGAGGTGCATAAT	891	QY	GENERAL INFORMATION:
1159	AGCCACGAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGACCGCGCTGGAGGTGCATAAT	1218	Db	APPLICANT: Xia, Yu-Ping et al.
892	GCCAAAGACAAAGCCCGGAGGACGAGTACAAACGACAGTACCGTGGTGGACGCTCCTC	951	QY	TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
1219	GCCAAAGACAAAGCCCGGAGGACGAGTACAAACGACAGTACCGTGGTGGACGCTCCTC	1378	Db	FILE REFERENCE: REG 710b
				CURRENT APPLICATION NUMBER: US/09/773,877B
				CURRENT FILING DATE: 2001-01-31
				NUMBER OF SEQ ID NOS: 27
				SOFTWARE: Patent in version 3.0



QY 952 ACCGTCCTGCACCAAGGCTGCTGAATGGCAAGGATACAGGTCAAGGTCTCCAAACAA 1011  
Db 1279 ACCGTCCTGCACCAAGGCTGCTGAATGGCAAGGATACAGGTCAAGGTCTCCAAACAA 1338  
QY 1012 GCCCTCCAGCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGGCCAGCCCGGAGAACCA 1071  
Db 1339 GCCCTCCAGCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGGCCAGCCCGGAGAACCA 1398  
QY 1072 CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGAGCTGACC 1131  
Db 1399 CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGAGCTGACC 1458  
QY 1132 TGCTCTGCTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCAG 1191  
Db 1459 TGCTCTGCTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCAG 1518  
QY 1192 CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTC 1251  
Db 1519 CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTC 1578  
QY 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCC 1638  
QY 1312 GTGATGATGAGGCTTGCACAAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGGT 1371  
Db 1639 GTGATGATGAGGCTTGCACAAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGGT 1698  
QY 1372 AAAAGA 1377  
Db 1699 AAAAGA 1704

## RESULT 9

US-08-227-496C-14  
; Sequence 14, Application US/08227496C  
; Patent No. 6130102

## GENERAL INFORMATION:

; APPLICANT: Greve, Jeffrey M.  
; APPLICANT: McClelland, Alan  
; TITLE OF INVENTION: Multimeric Forms of Human  
; TITLE OF INVENTION: Rhinovirus Receptor Protein  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bayer Corporation  
; STREET: 400 Morgan Lane  
; CITY: West Haven  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06516

## COMPUTER READABLE FORM:

; MEDIUM TYPE: diskette, 1.44 Mb storage  
; COMPUTER: Dell Optiplex GX1  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect 8.0 for Windows  
; CURRENT APPLICATION DATA:  
; FILING DATE: 04/14/94  
; APPLICATION NUMBER: US/08/227,496C

## CLASSIFICATION: 514

; PRIORITY INFORMATION DATA:  
; APPLICATION NUMBER: 07/903,069  
; FILING DATE: 06/22/92  
; APPLICATION NUMBER: 07/704,984  
; FILING DATE: 05/24/91  
; APPLICATION NUMBER: 07/556,238  
; FILING DATE: 07/20/90

## ATTORNEY/AGENT INFORMATION:

; NAME: Barbara A. Shimei  
; REGISTRATION NUMBER: 29,862  
; REFERENCE/DOCKET NUMBER: MTI 214.2C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203) 812-2786

; TELEFAX: (203) 812-5492  
; INFORMATION FOR SEQ ID NO: 14:

## SEQUENCE CHARACTERISTICS:

; LENGTH: 2043 bp  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; FEATURE:  
; NAME/KEY: tICAM(453)/IgG fusion  
; OTHER INFORMATION: bp 1-1359 = nucleotides coding  
; OTHER INFORMATION: for amino acid residues 1-453 of ICAM-1; bp 1360-  
; OTHER INFORMATION: 2040 = nucleotides coding for amino acid residues  
; OTHER INFORMATION: 216-442 of human heavy chain IgG1; bp 2401-2043 =  
; OTHER INFORMATION: stop codon  
; US-08-227-496C-14

Query Match 49.8%; Score 686; DB 3; Length 2043;

Best Local Similarity 95.9%; Pred. No. 1.6e-173;

Matches 704; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY	644	GTGGGCTGATGACCAAGAAACAGACACATTTGTGAGGGTCCATGAAAGACACAAACTC	703
Db	1310	GGGAGGTACCCGCAAGGTGACCGTGNATGTGTCTCTCCCCCGGTATGAGGACAAACTC	1369
QY	704	ACATATGCCACCGTCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCC	763
Db	1370	ACATATGCCACCGTCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCC	1429
QY	764	CCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGG	823
Db	1430	CCCCAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGG	1489
QY	824	TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGAGCGGTGAGG	883
Db	1490	TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGAGCGGTGAGG	1549
QY	884	TGCATATGCCAAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGTCA	943
Db	1550	TGCATATGCCAAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGTCA	1609
QY	944	GCCTCTCACCGTCTGCACACGAGCTGGCTGAATGCAAGAGGAGTACAAGTGAAGTCT	1003
Db	1610	GCCTCTCACCGTCTGCACACGAGCTGGCTGAATGCAAGAGGAGTACAAGTGAAGTCT	1669
QY	1004	CCAAAGAGCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC	1063
Db	1670	CCAAAGAGCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC	1729
QY	1064	GAGAACACAGGTGTACACCTGCCGCCCATTCGCGGGATGAGTGACCAAGAACAGGTCA	1123
Db	1730	GAGAACACAGGTGTACACCTGCCGCCCATTCGCGGGATGAGTGACCAAGAACAGGTCA	1789
QY	1124	GCCTGACCTGCTGTCAGAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGGAGACA	1183
Db	1790	GCCTGACCTGCTGTCAGAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGGAGACA	1849
QY	1184	ATGGGAGCCCGGAGAACCAACTACAAGACCAACGCTCCCGTGTCTGGAATCCGACGGCTCT	1243
Db	1850	ATGGGAGCCCGGAGAACCAACTACAAGACCAACGCTCCCGTGTCTGGAATCCGACGGCTCT	1909
QY	1244	TCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCGAGGTGGCAGAGGGGAAACGTCTCT	1303
Db	1910	TCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCGAGGTGGCAGAGGGGAAACGTCTCT	1969
QY	1304	CATGCTCCGCTGATGAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCCCTGT	1363
Db	1970	CATGCTCCGCTGATGAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCCCTGT	2029
QY	1364	CTCCGGGTAAATGA 1377	



Db 2030 CTCGGGGTAAATGA 2043

RESULT 10  
US-09-023-655-1223  
; Sequence 1223, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1223:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 705 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g243865  
US-09-023-655-1223

Query Match 49.7%; Score 684; DB 4; Length 705;  
Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCCCACCGTGGCCAGCACCTCATGATCTCCCGGACCCCTGAGGTCACA 813  
DB 5 GACAAACTCACATGCCCCACCGTGGCCAGCACCTCATGATCTCCCGGACCCCTGAGGTCACA 124  
QY 754 TTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 813  
DB 65 TTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 124  
QY 814 TGCGTGGTGGAGCGTAGGACCAAGACCTCATGAGGTCAGGTTCAACTGGTACGTGGAC 873  
DB 125 TGGCGTGGTGGAGCGTAGGACCAAGACCTCATGAGGTCAGGTTCAACTGGTACGTGGAC 184  
QY 874 GCGCGTAGGTCATTAATCCCAAGACAAAGCCGCGGAGGAGCAGTCAACACAGACCTGAC 933  
DB 185 GCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACACAGCCTGAC 244  
QY 934 CGTGTGGTCAGGCGTCTCAACCGTCTCCACACGAGGACTGGCTGAATGGCAAGGAGTCAAG 993

Db 245 CGTGTGGTCAGGCGTCTCAACCGTCTCGACCAAGGACTGGCTGAATGGCAAGGAGTCAAG 304

QY 994 TGCAGAGTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACCACTCTCCAAAGCCAAA 1053

Db 305 TGCAGAGTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACCACTCTCCAAAGCCAAA 364

QY 1054 GGGCAGCCCCGAGAACCAAGGTGTACACCTTGCCTCCCATCCCGGATAGCTGACCAAG 1113

Db 365 GGGCAGCCCCGAGAACCAAGGTGTACACCTTGCCTCCCATCCCGGATAGCTGACCAAG 424

QY 1114 AACAGGTACAGCTGACCTGCTGGTCAAGGGCTTCTATCCAGCGACATCCCGTGGAG 1173

Db 425 AACAGGTACAGCTGACCTGCTGGTCAAGGGCTTCTATCCAGCGACATCCCGTGGAG 484

QY 1174 TGGGAGAGCAATGGCGAGCCGAGAACCAACTACAAGACCAAGCTCCCGTGGCTGGACTCC 1233

Db 485 TGGGAGAGCAATGGCGAGCCGAGAACCAACTACAAGACCAAGCTCCCGTGGCTGGACTCC 544

QY 1234 GACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTTGGCAGCAGGGG 1293

Db 545 GACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTTGGCAGCAGGGG 604

QY 1294 AACGTCTTCTCATGCTCGGTGATCATGAGGCTCTGCAACCACTACACGCGAGAGAGC 1353

Db 605 AACGTCTTCTCATGCTCGGTGATCATGAGGCTCTGCAACCACTACACGCGAGAGAGC 664

QY 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377

Db 665 CTCTCCCTGTCTCCGGGTAAATGA 688

RESULT 11  
US-09-178-869-1  
; Sequence 1, Application US/09178869B  
; Patent No. 6197294  
; GENERAL INFORMATION:  
; APPLICANT: Tao, Weng  
; APPLICANT: Wong, Shou  
; APPLICANT: Hickey, William F.  
; APPLICANT: Hamman, Joseph P.  
; APPLICANT: Baetge, E. Edward  
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
; FILE REFERENCE: 17810-043  
; CURRENT APPLICATION NUMBER: US/09/178,869B  
; CURRENT FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1019  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1..)  
; OTHER INFORMATION: Description of Sequence: Recombinant  
; OTHER INFORMATION: Polynucleotide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)..(1008)  
US-09-178-869-1

Query Match 49.7%; Score 684; DB 3; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e-173;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCCCACCGTGGCCAGCACCTCATGATCTCCCGGACCCCTGAGGTCACA 813  
DB 328 GACAAACTCACATGCCCCACCGTGGCCAGCACCTCATGATCTCCCGGACCCCTGAGGTCACA 387  
QY 754 TTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 813  
DB 388 TTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 447





Db 1285 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 1344

Qy 1294 AACGTCTTCTCATGCTCGGTGATGATGAGGCTCTGCACAACCACTACACCGAAGAGC 1353

Db 1345 AACGTCTTCTCATGCTCGGTGATGATGAGGCTCTGCACAACCACTACACCGAAGAGC 1404

Qy 1354 CTCTCCCTGTCTCGGGTAAATGA 1377

Db 1405 CTCTCCCTGTCTCGGGTAAATGA 1428

RESULT 15

US-08-634-223-19

; Sequence 19, Application US/08634223

; Patent No. 5840298

; GENERAL INFORMATION:

; APPLICANT: BRAMS, Peter

; APPLICANT: CHAMAT, Soulaïma Salim

; APPLICANT: PAN, Li-Zhen

; APPLICANT: WALSH, Edward B.

; APPLICANT: HEARD, Cheryl Janne

; APPLICANT: NEWMAN, Roland Anthony

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/634,223

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,376

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/POCKET NUMBER: 012712-150

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1428 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1428

US-08-634-223-19

Query Match 49.7%; Score 684; DB 2; Length 1428;

Best Local Similarity 100.0%; Pred.No. 4.6e-173;

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 GACAAACTCACACTGCCCGGTGGACAAGCAGCTGAGGCTCTGCACAACCACTACACCGAAGAGC 753

Db 745 GACAAACTCACACTGCCCGGTGGACAAGCAGCTGAGGCTCTGCACAACCACTACACCGAAGAGC 804

Qy 754 TTCCTCTTCCCCCAAAACCAAGACACCCCTCATGATCTCCCGGACCCCTGAGGTGACA 813

Db 805 TTCTCTTCCCCCAAAACCAAGCACCCCTCATGATCTCCCGGACCCCTGAGTCACA 864

Qy 814 TGGGTGGTGGTGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 873

Db 865 TGGGTGGTGGTGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 924

Qy 874 GGGGTGGAGGTGCATANTGCACAAAGCCGGGAGGAGCAGTACACACGACACGTAC 933

Db 925 GGGGTGGAGGTGCATANTGCACAAAGCCGGGAGGAGCAGTACACACGACACGTAC 984

Qy 934 CGTGTGGTCAAGCGTCTCTCACCGTCTGCACAGGACTGGCTGTAATGCAAGGAGTACAAG 993

Db 985 CGTGTGGTCAAGCGTCTCTCACCGTCTGCACAGGACTGGCTGTAATGCAAGGAGTACAAG 1044

Qy 994 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053

Db 1045 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCAAAGCCAAA 1104

Qy 1054 GGGCAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113

Db 1105 GGGCAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1164

Qy 1114 AACGAGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCCGACATCGCGTGGAG 1173

Db 1165 AACGAGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCCGACATCGCGTGGAG 1224

Qy 1174 TGGGAGAGCAATGGGCAAGCCGGAGAACAACTACAAGACCAAGCTCCCGTGGTGGATCC 1233

Db 1225 TGGGAGAGCAATGGGCAAGCCGGAGAACAACTACAAGACCAAGCTCCCGTGGTGGATCC 1284

Qy 1234 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 1293

Db 1285 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 1344

Qy 1294 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACCGAAGAGC 1353

Db 1345 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACCGAAGAGC 1404

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Db 1405 CTCTCCCTGTCTCCGGGTAAATGA 1428

Search completed: August 27, 2005, 10:45:54

Job time : 253.401 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 22:22:41 ; Search time 960.42 Seconds  
(without alignments)  
9381.136 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1377	100.0	1377	10	US-09-773-877A-25
2	1377	100.0	1377	17	US-10-609-775-9
3	1377	100.0	1377	20	US-10-860-958-1
4	1377	100.0	1377	21	US-10-830-902-1
5	1377	100.0	1377	21	US-10-897-802-1
6	1377	100.0	1377	21	US-10-880-021-9
7	1377	100.0	1377	21	US-10-909-011-3

8	1377	100.0	1377	22	US-10-988-243-15	Sequence 15, Appl
9	1377	100.0	1377	24	US-11-016-097-15	Sequence 15, Appl
10	1328.4	96.5	1453	10	US-09-773-877A-21	Sequence 21, Appl
11	1328.4	96.5	1453	17	US-10-609-775-7	Sequence 7, Appl
12	1328.4	96.5	1453	21	US-10-880-021-7	Sequence 1, Appl
13	1328.4	96.5	1453	21	US-10-909-011-1	Sequence 11, Appl
14	1328.4	96.5	1453	22	US-10-988-243-11	Sequence 11, Appl
15	1328.4	96.5	1453	24	US-11-016-097-11	Sequence 12, Appl
16	1323.6	96.1	1377	21	US-10-855-559-12	Sequence 23, Appl
17	1049.2	76.2	1444	10	US-09-773-877A-23	Sequence 12, Appl
18	1049.2	76.2	1444	17	US-10-609-775-12	Sequence 12, Appl
19	1049.2	76.2	1444	21	US-10-880-021-12	Sequence 13, Appl
20	1049.2	76.2	1444	22	US-10-988-243-13	Sequence 13, Appl
21	1049.2	76.2	1444	24	US-11-016-097-13	Sequence 15, Appl
22	1039	75.5	1359	10	US-09-773-877A-15	Sequence 5, Appl
23	1039	75.5	1359	22	US-10-988-243-5	Sequence 5, Appl
24	1039	75.5	1359	24	US-11-016-097-5	Sequence 17, Appl
25	1032.4	75.0	1389	10	US-09-773-877A-17	Sequence 7, Appl
26	1032.4	75.0	1389	22	US-10-988-243-7	Sequence 7, Appl
27	1032.4	75.0	1389	24	US-11-016-097-7	Sequence 13, Appl
28	987.4	71.7	1674	10	US-09-773-877A-13	Sequence 3, Appl
29	987.4	71.7	1674	22	US-10-988-243-3	Sequence 3, Appl
30	987.4	71.7	1674	24	US-11-016-097-3	Sequence 19, Appl
31	982.4	71.3	1704	10	US-09-773-877A-19	Sequence 9, Appl
32	982.4	71.3	1704	22	US-10-988-243-9	Sequence 9, Appl
33	982.4	71.3	1704	24	US-11-016-097-9	Sequence 11, Appl
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35	980.8	71.2	1704	22	US-10-988-243-1	Sequence 1, Appl
36	980.8	71.2	1704	24	US-11-016-097-1	Sequence 7, Appl
37	687.8	49.9	1290	17	US-10-435-608-7	Sequence 7, Appl
38	687.8	49.9	1299	17	US-10-622-108-7	Sequence 9, Appl
39	687.8	49.9	1299	18	US-10-435-608-9	Sequence 9, Appl
40	687.8	49.9	1299	18	US-10-622-108-9	Sequence 9, Appl
41	687.2	49.9	1383	17	US-10-275-589-17	Sequence 31, Appl
42	687.2	49.9	1389	17	US-10-385-802-31	Sequence 29, Appl
43	687.2	49.9	1470	17	US-10-385-802-29	Sequence 27, Appl
44	687.2	49.9	1767	17	US-10-385-802-27	Sequence 23, Appl
45	687.2	49.9	1947	17	US-10-385-802-23	

ALIGNMENTS

RESULT 1

US-09-773-877A-25  
; Sequence 25, Application US/09773877A  
; Publication No. US20030017977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773.877A  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor  
; NAME/KEY: CDS  
; LOCATION: (1)..(1377)  
US-09-773-877A-25

Query Match 100.0%; Score 1377; DB 10; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2
US-10-609-775-9
; Sequence 9, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Daly
; APPLICANT: James P. Fandl
; APPLICANT: Nicholas J. Papadopoulos
; TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: REG 710D
; CURRENT APPLICATION NUMBER: US/10/609,775
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 3

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US-10-860-958-1
; Sequence 1, Application US/10860958
; Publication No. US20040265309A1
; GENERAL INFORMATION:
; APPLICANT: Handel, Jessica
; APPLICANT: Hodelash, Jocelyn
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; APPLICANT: Yamashiro, Darrell
; APPLICANT: Huang, Jianzhong
; APPLICANT: Yancopoulos, George
; APPLICANT: Rudge, John
; TITLE OF INVENTION: Method of Tumor Regression with VEGF
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: REG 714A
; CURRENT APPLICATION NUMBER: US/10/860,958
; PRIOR FILING DATE: 2004-06-04
; PRIOR FILING DATE: 60/476,425
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 841 GACCTGAGGTCAAGTTCAATGCTGACGTGACGCGCGTGGAGGTGCATAATGCCAAGACA 900
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Qy 1201 AACTACAGACACGCTCCGCTGCTGACCTCCGAGCTCCGAGCTCTCTCTCTACAGCAAG 1260
Db 1201 AACTACAGACACGCTCCGCTGCTGACCTCCGAGCTCCGAGCTCTCTCTCTACAGCAAG 1260
Qy 1261 CTCACCTGGCAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGCTGATGCAT 1320
Db 1261 CTCACCTGGCAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGCTGATGCAT 1320
Qy 1321 GAGCTCTGCAACCACTACACGCGAAGAGCTCTCCCTGTCTCCGGTAAATGA 1377
Db 1321 GAGCTCTGCAACCACTACACGCGAAGAGCTCTCCCTGTCTCCGGTAAATGA 1377

RESULT 4
US-10-830-902-1
; Sequence 1, Application US/10830902
; Publication No. US20050004027A1
; GENERAL INFORMATION:
; APPLICANT: Stanley Wiegand
; APPLICANT: Jingtai Cao
; APPLICANT: Claus Cursiefen
; TITLE OF INVENTION: Method of Treating Corneal Transplant
; FILE REFERENCE: REG 713B
; CURRENT APPLICATION NUMBER: US/10/830,902
; CURRENT FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-830-902-1
Query Match 100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGGCGCTGCTCAGCTGCTGCTTCTC 60
Db 1 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGGCGCTGCTCAGCTGCTGCTTCTC 60
Qy 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
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Db 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Qy 121 CCCGAAATTATACACATGACTGAAGGAAGGAGCTCGTCAATCCCTCCCGGTTCACGTCA 180
Db 121 CCCGAAATTATACACATGACTGAAGGAAGGAGCTCGTCAATCCCTCCCGGTTCACGTCA 180
Qy 181 CCTAACATCATCTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAA 240
Db 181 CCTAACATCATCTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAA 240
Qy 241 CGCATATCTGGGACAGTACGAAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA 300
Db 241 CGCATATCTGGGACAGTACGAAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA 300
Qy 301 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCATTTGTATAGACAAAATATCTCACA 360
Db 301 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCATTTGTATAGACAAAATATCTCACA 360
Qy 361 CATCGACAAAACCAATACAATCATAGATGTGGTTCGTGAGTCCGTCTCATGGAATTGAAC 420
Db 361 CATCGACAAAACCAATACAATCATAGATGTGGTTCGTGAGTCCGTCTCATGGAATTGAAC 420
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGAT 480
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGAT 480
Qy 481 GACTTCAACTGGGAATACCTTTCTCGAAGCATCAGCATAGAAACTTTGTAACCCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTTCTCGAAGCATCAGCATAGAAACTTTGTAACCCGAGAC 540
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACCACTTAACTATAGATGGT 600
Db 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACCACTTAACTATAGATGGT 600
Qy 601 GTAAACCCGAGTGACCAAGGATTTGTACACCTGTGACAGTCCAGTGGGCTGATGACCAAG 660
Db 601 GTAAACCCGAGTGACCAAGGATTTGTACACCTGTGACAGTCCAGTGGGCTGATGACCAAG 660
Qy 661 AAGAACAGCACTTTGTGAGGGTCCATGAAAGAGCAAAACTCACATGCCCAACCGTGC 720
Db 661 AAGAACAGCACTTTGTGAGGGTCCATGAAAGAGCAAAACTCACATGCCCAACCGTGC 720
Qy 721 CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAGGAC 780
Db 721 CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAGGAC 780
Qy 781 ACCCTCATGATCTCCCGACCCCTGAGGTCAATGCTGGTGGTGGAGCTGAGCCACGAA 840
Db 781 ACCCTCATGATCTCCCGACCCCTGAGGTCAATGCTGGTGGTGGAGCTGAGCCACGAA 840
Qy 841 GACCTGAGGTCAAGTTCAACTGGTACGTGACGCGCGTGGAGGTGCATAATGCCAAGACA 900
Db 841 GACCTGAGGTCAAGTTCAACTGGTACGTGACGCGCGTGGAGGTGCATAATGCCAAGACA 900
Qy 901 AAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTTCAGCGTCTCACCGTCTCTG 960
Db 901 AAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTTCAGCGTCTCACCGTCTCTG 960
Qy 961 CACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAAAGCCCTCCA 1020
Db 961 CACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAAAGCCCTCCA 1020
Qy 1021 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTAC 1080
Db 1021 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTAC 1080
Qy 1081 ACCCTGCCCATCCCGGATGAGCTGACCAAGAACACAGGTTCAGCTGACCTGCTGCTC 1140
Db 1081 ACCCTGCCCATCCCGGATGAGCTGACCAAGAACACAGGTTCAGCTGACCTGCTGCTC 1140
Qy 1141 AAAGCTTCTATCCAGCGACATGCCGTGAGTGGAGAGCAATGGGACGCCGGAGAAC 1200
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Db 1141 AAAGCTTCTATCCAGCGACATCCCGTGGAGTGGAGCAATGGCAGCGGAGAAC 1200  
Qy 1201 AACTACAAGACCAACCCCTCCGCTGCTGAGCTCCGAGCGCTCTCTTCTCTACAGCAAG 1260  
Db 1201 AACTACAAGACCAACCCCTCCGCTGCTGAGCTCCGAGCGCTCTCTTCTCTACAGCAAG 1260  
Qy 1261 CTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGCTGATGCAT 1320  
Db 1261 CTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCCGCTGATGCAT 1320  
Qy 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377

## RESULT 5

US-10-897-802-1  
; Sequence 1, Application US/10897802  
; Publication No. US20050032699A1  
; GENERAL INFORMATION:  
; APPLICANT: Jocelyn Holash  
; APPLICANT: Robert Jaffe  
; APPLICANT: Limin Hu  
; APPLICANT: George D. Yancopoulos  
; TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent  
; FILE REFERENCE: REG 715B  
; CURRENT APPLICATION NUMBER: US/10/897,802  
; CURRENT FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: 60/493,971  
; PRIOR FILING DATE: 2003-08-08  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-897-802-1

Query Match 100.0%; Score 1377; DB 21; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTCAGCTACTTGGGACACCGGGGCTCTGCTGTGCGGCTGCTCAGCTGTCTGCTTCTC 60  
Db 1 ATGCTCAGCTACTTGGGACACCGGGGCTCTGCTGTGCGGCTGCTCAGCTGTCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTA CAGTGAATC 120  
Db 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTA CAGTGAATC 120  
Qy 121 CCGGAAATATATACATGACTGAAAGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180  
Db 121 CCGGAAATATATACATGACTGAAAGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180  
Qy 181 CCTAACATCACTGTATTCTTTAAAGAGTTTCCACTTGACACTTTTGATCCCTGATGGGAAA 240  
Db 181 CCTAACATCACTGTATTCTTTAAAGAGTTTCCACTTGACACTTTTGATCCCTGATGGGAAA 240  
Qy 241 CGCATATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA 300  
Db 241 CGCATATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA 300  
Qy 301 GGGCTTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTATAGACAACTATCTACA 360  
Db 301 GGGCTTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTATAGACAACTATCTACA 360  
Qy 361 CATGCACAAACCAATACATATAGATGTGTCTGAGTCCGTCTCATGGAAATGAACTA 420  
Db 361 CATGCACAAACCAATACATATAGATGTGTCTGAGTCCGTCTCATGGAAATGAACTA 420  
Qy 421 TCTGTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480  
Db 421 TCTGTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480

Qy 481 GACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAGAAACTTTGTAACCCGAGAC 540  
Db 481 GACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAGAAACTTTGTAACCCGAGAC 540  
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAAATTTTGTAGCACCTTAACTATAGATGGT 600  
Db 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAAATTTTGTAGCACCTTAACTATAGATGGT 600  
Qy 601 GTAAACCCGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 601 GTAAACCCGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Qy 661 AAGAAACAGCACATTTGTTCAGGGTCCATGAAAGAGCAAAACTCACAATGTCACCGGTGC 720  
Db 661 AAGAAACAGCACATTTGTTCAGGGTCCATGAAAGAGCAAAACTCACAATGTCACCGGTGC 720  
Qy 721 CCAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
Db 721 CCAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 841 GACCTGAGGTCAAGTTCAACTGCTGACGCGGTGGAGGTGCAATAATGCCAAGACA 900  
Db 841 GACCTGAGGTCAAGTTCAACTGCTGACGCGGTGGAGGTGCAATAATGCCAAGACA 900  
Qy 901 AAGCCGCGGGAGGAGCAGTACAAACAGCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Db 901 AAGCCGCGGGAGGAGCAGTACAAACAGCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
Qy 961 CACGAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTTCCCA 1020  
Db 961 CACGAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTTCCCA 1020  
Qy 1021 GCGCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGCTGTAC 1080  
Db 1021 GCGCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAACAGCTGTAC 1080  
Qy 1081 ACCCTGCCCCCATCTCCCGGATGAGTCAACCAAGAACAGGTGACCTGCTGCTGCTGCTG 1140  
Db 1081 ACCCTGCCCCCATCTCCCGGATGAGTCAACCAAGAACAGGTGACCTGCTGCTGCTGCTG 1140  
Qy 1141 AAGGCTTCTATCCACGACATCCCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAAC 1200  
Db 1141 AAGGCTTCTATCCACGACATCCCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAAC 1200  
Qy 1201 AACTACAAGACCAACCGCTCCGCTGCTGAGTCCGAGCGCTCTTCTTCTTCTTCTTCTTCT 1260  
Db 1201 AACTACAAGACCAACCGCTCCGCTGCTGAGTCCGAGCGCTCTTCTTCTTCTTCTTCTTCT 1260  
Qy 1261 CTCAACCTGGACAAAGAGCAGGTGGCAGCGGGAAACGTCTTCTCATGCTCCGCTGATGCAT 1320  
Db 1261 CTCAACCTGGACAAAGAGCAGGTGGCAGCGGGAAACGTCTTCTCATGCTCCGCTGATGCAT 1320  
Qy 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377

## RESULT 6

US-10-880-021-9  
; Sequence 9, Application US/10880021  
; Publication No. US20050043236A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Fandl, James P.  
; APPLICANT: Papadopoulos, Nicholas J.  
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof  
; FILE REFERENCE: RGE 710D2  
; CURRENT APPLICATION NUMBER: US/10/880,021

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; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-880-021-9

Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCTAGCTACTGGGACACCGGGTCTGTGTGCGCGTGTCTGAGAGTGTACAGTGAATC 120
Db 1 ATGTCTAGCTACTGGGACACCGGGTCTGTGTGCGCGTGTCTGAGAGTGTACAGTGAATC 60
Qy 61 ACAGGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120
Db 61 ACAGGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120
Qy 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTTCCTCCCTGCGGGTTACGTCA 180
Db 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTTCCTCCCTGCGGGTTACGTCA 180
Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240
Db 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGAATGCAACGTACAAAGAATA 300
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGAATGCAACGTACAAAGAATA 300
Qy 301 GGGATTCAGCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGCAAACTCTCACA 360
Db 301 GGGATTCAGCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGCAAACTCTCACA 360
Qy 361 CATGACAAACCAATACAAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAAATGAAC 420
Db 361 CATGACAAACCAATACAAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAAATGAAC 420
Qy 421 TCTGTTGAGAAAGCTTGCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGAT 480
Db 421 TCTGTTGAGAAAGCTTGCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGAT 480
Qy 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540
Qy 541 CTAAGAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600
Db 541 CTAAGAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600
Qy 601 GTAACCCGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAACCCGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Qy 661 AAGAACAGCATTTGTCCAGGCTCCATGAAAGGACAAACTCAGCATGCCACCGTGC 720
Db 661 AAGAACAGCATTTGTCCAGGCTCCATGAAAGGACAAACTCAGCATGCCACCGTGC 720
Qy 721 CCAGCACCTGAACCTCTGGGGGAGCCGTGAGTCAATGCTGCTTCTTCCCTCCCAAAACCAAGGAC 780
Db 721 CCAGCACCTGAACCTCTGGGGGAGCCGTGAGTCAATGCTGCTTCTTCCCTCCCAAAACCAAGGAC 780
Qy 781 ACCCTCATGATCTCCCGAACCCCTGAGTCAATGCTGCTGCTGCTGAGTGAAGCAAGAA 840
Db 781 ACCCTCATGATCTCCCGAACCCCTGAGTCAATGCTGCTGCTGCTGAGTGAAGCAAGAA 840
Qy 841 GACCTGAGGTCAAGTTCAACTGGTACGTGAGCGCGGTGGAGGTGCATTAATGCCAAGACA 900
Db 841 GACCTGAGGTCAAGTTCAACTGGTACGTGAGCGCGGTGGAGGTGCATTAATGCCAAGACA 900

; Sequence 3, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Holash
; APPLICANT: George Yancopoulos
; APPLICANT: Phyllis R. Wacheberger
; APPLICANT: Adam P. Dicker
; APPLICANT: Randy Burd
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/492,864
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-909-011-3

Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCTAGCTACTGGGACACCGGGTCTGTGTGCGCGTGTCTGAGAGTGTACAGTGAATC 60
Db 1 ATGTCTAGCTACTGGGACACCGGGTCTGTGTGCGCGTGTCTGAGAGTGTACAGTGAATC 60
Qy 61 ACAGGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120
Db 61 ACAGGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120
Qy 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTTCCTCCCTGCGGGTTACGTCA 180
Db 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTTCCTCCCTGCGGGTTACGTCA 180
Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240
Db 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGAATGCAACGTACAAAGAATA 300
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGAATGCAACGTACAAAGAATA 300
Qy 301 GGGATTCAGCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGCAAACTCTCACA 360
Db 301 GGGATTCAGCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGCAAACTCTCACA 360
Qy 361 CATGACAAACCAATACAAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAAATGAAC 420
Db 361 CATGACAAACCAATACAAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAAATGAAC 420
Qy 421 TCTGTTGAGAAAGCTTGCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGAT 480
Db 421 TCTGTTGAGAAAGCTTGCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGAT 480
Qy 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540
Qy 541 CTAAGAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600
Db 541 CTAAGAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600
Qy 601 GTAACCCGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAACCCGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Qy 661 AAGAACAGCATTTGTCCAGGCTCCATGAAAGGACAAACTCAGCATGCCACCGTGC 720
Db 661 AAGAACAGCATTTGTCCAGGCTCCATGAAAGGACAAACTCAGCATGCCACCGTGC 720
Qy 721 CCAGCACCTGAACCTCTGGGGGAGCCGTGAGTCAATGCTGCTTCTTCCCTCCCAAAACCAAGGAC 780
Db 721 CCAGCACCTGAACCTCTGGGGGAGCCGTGAGTCAATGCTGCTTCTTCCCTCCCAAAACCAAGGAC 780
Qy 781 ACCCTCATGATCTCCCGAACCCCTGAGTCAATGCTGCTGCTGCTGAGTGAAGCAAGAA 840
Db 781 ACCCTCATGATCTCCCGAACCCCTGAGTCAATGCTGCTGCTGCTGAGTGAAGCAAGAA 840
Qy 841 GACCTGAGGTCAAGTTCAACTGGTACGTGAGCGCGGTGGAGGTGCATTAATGCCAAGACA 900
Db 841 GACCTGAGGTCAAGTTCAACTGGTACGTGAGCGCGGTGGAGGTGCATTAATGCCAAGACA 900
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Db 121 CCAGAAATTTATACATGCTGAAGGAAGGAGCTCGTCATTCCCTCGCGGGTTACGTCA 180  
Qy 181 CTTAACATCAGCTTTACTTTAAAGATTTTCCACTTGTGACACTTTTCATCCCTGATGAAAA 240  
Db 181 CTTAACATCAGCTTTACTTTAAAGATTTTCCACTTGTGACACTTTTCATCCCTGATGAAAA 240  
Qy 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA 300  
Db 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA 300  
Qy 301 GGGCTTCTGACCTGTGAAGCAACGTCATATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Db 301 GGGCTTCTGACCTGTGAAGCAACGTCATATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Db 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480  
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480  
Qy 481 GACTTCAACTGGGAATACCTTCTTTCGAGCATCAGCATAGAACTTTGTAAACCGAGAC 540  
Db 481 GACTTCAACTGGGAATACCTTCTTTCGAGCATCAGCATAGAACTTTGTAAACCGAGAC 540  
Qy 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCGAGCACTTAATATAGATGGT 600  
Db 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCGAGCACTTAATATAGATGGT 600  
Qy 601 GTAAACCCGAGTGACCAAGGATTTGACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 601 GTAAACCCGAGTGACCAAGGATTTGACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Qy 661 AAGBACAGACATTTTGTGAGGTTCATGAAAGGACAAACTCACAATGCCACCGTGC 720  
Db 661 AAGBACAGACATTTTGTGAGGTTCATGAAAGGACAAACTCACAATGCCACCGTGC 720  
Qy 721 CCAGCACTGAACCTCTGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCCAAGGAC 780  
Db 721 CCAGCACTGAACCTCTGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCCAAGGAC 780  
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTTCATGCGTGGTGGAGCGTGAGCCACGAA 840  
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTTCATGCGTGGTGGAGCGTGAGCCACGAA 840  
Qy 841 GACCTGAGGTCAAGTTCACTGTGACGCGCGTGAGAGTGATCAATGCCAAGACA 900  
Db 841 GACCTGAGGTCAAGTTCACTGTGACGCGCGTGAGAGTGATCAATGCCAAGACA 900  
Qy 901 AAGCCGGGAGGAGCAGTACAAACGACGTCACGCTGTGCTCAGCGTCTCAGCGTCTG 960  
Db 901 AAGCCGGGAGGAGCAGTACAAACGACGTCACGCTGTGCTCAGCGTCTCAGCGTCTG 960  
Qy 961 CAACAGGACTGGCTGAAATGGCAAGGATACAAAGTCAAGTCAAGGCTCTCCAAAGCCCTCCA 1020  
Db 961 CAACAGGACTGGCTGAAATGGCAAGGATACAAAGTCAAGTCAAGGCTCTCCAAAGCCCTCCA 1020  
Qy 1021 GCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGAC 1080  
Db 1021 GCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGAC 1080  
Qy 1081 ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTGTC 1140  
Db 1081 ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTGTC 1140  
Qy 1141 AAAGGCTTTCTATCCAGAGCATCCGCGTGGAGTGAGAGCAATGGGACGCCGAGAAC 1200  
Db 1141 AAAGGCTTTCTATCCAGAGCATCCGCGTGGAGTGAGAGCAATGGGACGCCGAGAAC 1200  
Qy 1201 AACTACAAGACACGCTCCCGTGTGATGATCCGAGCGGCTCTTCTTCTCTACAGCAAG 1260  
Db 1201 AACTACAAGACACGCTCCCGTGTGATGATCCGAGCGGCTCTTCTTCTCTACAGCAAG 1260

## RESULT 8

US-10-988-243-15  
; Sequence 15, Application US/10988243  
; Publication No. US20050175610A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiegand, Stanley  
; APPLICANT: Papadopoulos, Nicholas J.  
; APPLICANT: Yancopoulos, George  
; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinetic Properties  
; TITLE OF INVENTION: and Methods of Making and Using Thereof  
; FILE REFERENCE: REG 710P  
; CURRENT APPLICATION NUMBER: US/10/988,243  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: 10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-988-243-15

Query Match 100.0%; Score 1377; DB 22; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGCTGCTTCTC 60  
Db 1 ATGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Qy 121 CCGGAAATTTATACATGACTGAAGGAAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180  
Db 121 CCGGAAATTTATACATGACTGAAGGAAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180  
Qy 181 CCTAACATCACTGTTACTTTTAAAGATTTTCCACTTGACACTTTGATCCCTGATGAAAA 240  
Db 181 CCTAACATCACTGTTACTTTTAAAGATTTTCCACTTGACACTTTGATCCCTGATGAAAA 240  
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA 300  
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA 300  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Db 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Db 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480  
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480

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Qy 481 GACTTCAACTGGGAATACCTCTTCTCGAAGCATCAGCATAGAAACCTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTCTTCTCGAAGCATCAGCATAGAAACCTGTAAACCGAGAC 540
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600
Db 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600
Qy 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGGAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGGAGCATCCAGTGGGCTGATGACCAAG 660
Qy 661 AAGAACAGCACAATTTGTCCAGGCTCATGAAAGAGCAAACTCACATGCCACCTGTC 720
Db 661 AAGAACAGCACAATTTGTCCAGGCTCATGAAAGAGCAAACTCACATGCCACCTGTC 720
Qy 721 CCAGCACCTGAACTCTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
Db 721 CCAGCACCTGAACTCTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGTGGACGTGAGCCAGAA 840
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGTGGACGTGAGCCAGAA 840
Qy 841 GACCTGAGGTCAAGTTCAACTGTGTGAGCGCGTGGAGGTGCATTAATGCCAAGACA 900
Db 841 GACCTGAGGTCAAGTTCAACTGTGTGAGCGCGTGGAGGTGCATTAATGCCAAGACA 900
Qy 901 AAGCGCGGGAGGAGCAGTACAAACGACGCTACCGTGTGTGTCAGCGTCTCCACCGTCTG 960
Db 901 AAGCGCGGGAGGAGCAGTACAAACGACGCTACCGTGTGTGTCAGCGTCTCCACCGTCTG 960
Qy 961 CACGAGACTGGCTGAATGGCAAGGATPACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1020
Db 961 CACGAGACTGGCTGAATGGCAAGGATPACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1020
Qy 1021 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1080
Db 1021 GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1080
Qy 1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCTGCTC 1140
Db 1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCTGCTC 1140
Qy 1141 AAAGGCTTCTATCCAGGACATCGCGTGAGTGGAGAGCAATGGGCGAGCCGGAGAAC 1200
Db 1141 AAAGGCTTCTATCCAGGACATCGCGTGAGTGGAGAGCAATGGGCGAGCCGGAGAAC 1200
Qy 1201 AACTACAAGACCAAGCTCCCGTGTGAGCTCCGACGCGCTCTTCTTCTTCTTCTACAGCAAG 1260
Db 1201 AACTACAAGACCAAGCTCCCGTGTGAGCTCCGACGCGCTCTTCTTCTTCTTCTACAGCAAG 1260
Qy 1261 CTCACCGTGGACAAGAGCAGGTGGCAGCGGGAAAGCTTCTTCTCATGCTCCGATGATGCAT 1320
Db 1261 CTCACCGTGGACAAGAGCAGGTGGCAGCGGGAAAGCTTCTTCTCATGCTCCGATGATGCAT 1320
Qy 1321 GAGGCTCTGCACACCACTACACGAGAGGCTCTCCCTGTCTCCGGTAAATGA 1377
Db 1321 GAGGCTCTGCACACCACTACACGAGAGGCTCTCCCTGTCTCCGGTAAATGA 1377
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## RESULT 9

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US-11-016-097-15
; Sequence 15, Application US/11016097
; Publication No. US20050163798A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,097
; CURRENT FILING DATE: 2004-12-17
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; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1374)
US-11-016-097-15
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Query Match 100.0%; Score 1377; DB 24; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTCAGCTACTGGGACACCGGGGCTCCTGCTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60
Db 1 ATGCTCAGCTACTGGGACACCGGGGCTCCTGCTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60
Qy 61 ACAGGATCTAGTTCCGGAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Db 61 ACAGGATCTAGTTCCGGAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Qy 121 CCCGAATATTATACATGACTGAAAGGAGGCTGCTCAATCCCTGCCGGGTACGTCA 180
Db 121 CCCGAATATTATACATGACTGAAAGGAGGCTGCTCAATCCCTGCCGGGTACGTCA 180
Qy 181 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTTGGACCTTTGATCCCTGATGGAAA 240
Db 181 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTTGGACCTTTGATCCCTGATGGAAA 240
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAAGCTACAAGAAATA 300
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAAGCTACAAGAAATA 300
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 360
Db 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 360
Qy 361 CATCGACAAACCAATCAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACATA 420
Db 361 CATCGACAAACCAATCAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACATA 420
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATT 480
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATT 480
Qy 481 GACTTCAACTGGGAATACCTCTTCCGAGCATCAGCATAGAAACTTTGTAAACCCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTCTTCCGAGCATCAGCATAGAAACTTTGTAAACCCGAGAC 540
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGGT 600
Db 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGGT 600
Qy 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGGAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGGAGCATCCAGTGGGCTGATGACCAAG 660
Qy 661 AAGAACAGCACAATTTGTCCAGGCTCATGAAAGAGCAAAACTCACATGCCACCTGTC 720
Db 661 AAGAACAGCACAATTTGTCCAGGCTCATGAAAGAGCAAAACTCACATGCCACCTGTC 720
Qy 721 CCAGCACCTGAACTCTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
Db 721 CCAGCACCTGAACTCTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
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US-10-980-021-7
; Sequence 7, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: Pandopoulos, Nicholas J.
; APPLICANT: Papadopoulos, Nicholas J.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
; FILE REFERENCE: RGE 710D2
; CURRENT APPLICATION NUMBER: US/10/880,021
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-980-021-7

Query Match          96.5%; Score 1328.4; DB 21; Length 1453;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 3

Qy 1 ATGCTCAGCTACTGGGACACCGGGGTCTGCTGTGCGGCTGCTCAGCTGTGCTGCTTC 60
Db |||
Qy 61 ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120
Db |||
Qy 129 ACAGGATCTAGTTCGGA-----GGTAGACCTTTCGTAGAGATGTACAGTGAATC 179
Db |||
Qy 121 CCCGAAATTATACATGACTGAAGGAGGAGCTGCTCATTCCTCCGCGGTACGTC 180
Db |||
Qy 180 CCCGAAATTATACATGACTGAGGAGGAGCTGCTCATTCCTCCGCGGTACGTC 239
Db |||
Qy 181 CCTAACATCAGCTTTACTTTAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 240
Db |||
Qy 240 CCTAACATCAGCTTTACTTTAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 299
Db |||
Qy 241 CGCATTAATCTGGGACAGTAGAAGGGCTTCATCATATCAAATGCAAGTACAAAGAAATA 300
Db |||
Qy 300 CGCATTAATCTGGGACAGTAGAAGGGCTTCATCATATCAAATGCAAGTACAAAGAAATA 359
Db |||
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATAGA CAAACTATCTCA 360
Db |||
Qy 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATAGA CAAACTATCTCA 419
Db |||
Qy 361 CATCGAACCAATACATCATAGATCTGGTCTTGAGTCGCTCATGAAATTGAACTA 420
Db |||
Qy 420 CATCGAACCAATACATCATAGATCTGGTCTTGAGTCGCTCATGAAATTGAACTA 479
Db |||
Qy 421 TCTGTTGGAGAAAAGCTTGCTTTAAATTTGTACAGCAAGAACTGAACTTAAATGTGGGGATT 480
Db |||
Qy 480 TCTGTTGGAGAAAAGCTTGCTTTAAATTTGTACAGCAAGAACTGAACTTAAATGTGGGGATT 539
Db |||
Qy 481 GACTTCAA CTGGGAATA CCGTTCTTCGAGCATCAGCATAGA AACTTGTGTAAC CCGAGAC 540
Db |||
Qy 540 GACTTCAA CTGGGAATA CCGTTCTTCGAGCATCAGCATAGA AACTTGTGTAAC CCGAGAC 599
Db |||
Qy 541 CTAAAAACCCAGCTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGT 600
Db |||
Qy 600 CTAAAAACCCAGCTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGT 659
Db |||
Qy 601 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db |||
Qy 660 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
Db |||
Qy 661 AAGAACAGCACATTTGTGACGGGTCCATGAAAG-----GACAAAACCTCAACATGC 711
Db |||
Qy 720 AAGAACAGCACATTTGTGACGGGTCCATGAAAGGGCCCGGGCGCAAAAACCTCAACATGC 779

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Query Match		96.5%;	Score 1328.4;	DB 21;	Length 1453;
Best Local Similarity		98.6%;	Pred. No. 0;		
Matches 1367;		Conservative	0;	Mismatches	1; Indels 18; Gaps 2;
Qy	1	ATGTCAGCTACTGGGACACCGGGTCTCTGTGCGCGTCTCAGCTGTCTGCTTCTC	60		
Db	69	ATGGTCAGCTACTGGGACACCGGGTCTCTGTGTGCGCGTCTCAGCTGTCTGCTTCTC	128		
Qy	61	ACAGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC	120		
Db	129	ACAGATCTAGTTCGGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC	179		
Qy	121	CCCGAAATTATACACATGACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGGTTACGTCA	180		
Db	180	CCCGAAATTATACATGACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGGTTACGTCA	239		
Qy	181	CCTAACATCACTGTTTACCTTTAAAAAGTTTCCACTTGGACACTTTGATCCCTGATGGAAA	240		
Db	240	CCTAACATCACTGTTTACCTTTAAAAAGTTTCCACTTGGACACTTTGATCCCTGATGGAAA	299		
Qy	241	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAATA	300		
Db	300	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAATA	359		
Qy	301	GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA	360		
Db	360	GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA	419		
Qy	361	CATGCAAAACCAATACATAGATGGTCTCTGAGTCCGTCTCTGGAATTTGAACATA	420		
Db	420	CATGCAAAACCAATACATAGATGGTCTCTGAGTCCGTCTCTGGAATTTGAACATA	479		
Qy	421	TCTGTGAGAAAAGCTTGTCTTAAATTGTTACAGCAAGAACTGAACTAAATGTGGGATT	480		
Db	480	TCTGTGAGAAAAGCTTGTCTTAAATTGTTACAGCAAGAACTGAACTAAATGTGGGATT	539		
Qy	481	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAAACTTGTAAACCGAGAC	540		
Db	540	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAAACTTGTAAACCGAGAC	599		
Qy	541	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGT	600		
Db	600	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGT	659		
Qy	601	GTAACCCGGAGTACCAGGATTTGTACACCTGTGCGAGCATCCAGTGGCTGATGACCAAG	660		
Db	660	GTAACCCGGAGTACCAGGATTTGTACACCTGTGCGAGCATCCAGTGGCTGATGACCAAG	719		
Qy	661	AAGAACAGACATTTGTGAGGTCCATGAAAAG-----GACAAACTCACACATGC	711		
Db	720	AAGAACAGACATTTGTGAGGTCCATGAAAAGGGCCCGGGCGAATAACTCACACATGC	779		
Qy	712	CCACCGTGCCGACGACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCCCCCAGAAA	771		
Db	780	CCACCGTGCCGACGACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTTCCCCCAGAAA	839		
Qy	772	CCCAAGGACCCCTCATGATCTCCGGACCCCTGAGGTCAATGGTGGTGGTGGAGCGTG	831		
Db	840	CCCAAGGACCCCTCATGATCTCCGGACCCCTGAGGTCAATGGTGGTGGTGGAGCGTG	899		
Qy	832	AGCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT	891		
Db	900	AGCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT	959		
Qy	892	GCCAAGCAAAAGCCCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTC	951		
Db	960	GCCAAGCAAAAGCCCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTC	1019		
Qy	952	ACCGTCTCTGACAGGACTGCTGAAATGGCAAGGATCAAGTGCAGGCTCTCAACAAA	1011		
Db	1020	ACCGTCTCTGACAGGACTGCTGAAATGGCAAGGATCAAGTGCAGGCTCTCAACAAA	1079		
Qy	1012	GCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA	1071		

Db	1080																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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Db 240 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAAAA 299  
Qy 241 CGATAAATCTGGGACAGTAGAAGGCTTTCATCATATCAAAATGCAACGTCACAAAGAAATA 300  
Db 300 CGCATATCTGGGACAGTAGAAGGCTTTCATCATATCAAAATGCAACGTCACAAAGAAATA 359  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCAATTTGTATAAGACAAACTATCTACA 360  
Db 360 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCAATTTGTATAAGACAAACTATCTACA 419  
Qy 361 CATGACAAACCAATACATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 420  
Db 420 CATGACAAACCAATACATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 479  
Qy 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACATAAATGTGGGATT 480  
Db 480 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACATAAATGTGGGATT 539  
Qy 481 GACTTCAACTGGGAATACCCCTTCTCGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540  
Db 540 GACTTCAACTGGGAATACCCCTTCTCGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 599  
Qy 541 CTNAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCAGCACCTTAACCTATAGATGT 600  
Db 600 CTNAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCAGCACCTTAACCTATAGATGT 659  
Qy 601 GTAAACCCGAGTGACCAAGGATTGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660  
Db 660 GTAAACCCGAGTGACCAAGGATTGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 719  
Qy 661 AAGAACAGCACATTTGTCCAGGTCATGAAAG-----GACAAACTTCACACATGC 711  
Db 720 AAGAACAGCACATTTGTCCAGGTCATGAAAGGGCCCGGGCGACAAAACTTCACACATGC 779  
Qy 712 CCACGCTCCAGCACCTGAACTCTCGGGGAGCGCTCAGTCTTCTCTTCCCGCCAAA 771  
Db 780 CCACGCTCCAGCACCTGAACTCTCGGGGGAGCGCTCAGTCTTCTCTTCCCGCCAAA 839  
Qy 772 CCCAAGGACACCTCATCATCTCCCGGACCCCTGAGGTACATGCGTGGTGTGAGCGTG 831  
Db 840 CCCAAGGACACCTCATCATCTCCCGGACCCCTGAGGTACATGCGTGGTGTGAGCGTG 899  
Qy 832 AGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTACGCGGCGGTGGAGGTGCATAAT 891  
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US-11-016-097-11  
; Sequence 11, Application US/11016097  
; Publication No. US20050163798A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING THEREOF  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,097  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
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; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 1453  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1442)  
US-11-016-097-11

Query Match 96.5%; Score 1328.4; DB 24; Length 1453;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;  
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